

## SEQUENCE LISTING

<110> Barbet, Anthony F.  
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<120> Ehrlichia Ruminantium Polypeptides, Antigens, Polynucleotides, and  
Methods of Use

<130> UF-299XC1

<150> US 60/269,944

<151> 2001-02-20

<160> 117

<170> PatentIn version 3.1

<210> 1

<211> 278

<212> PRT

<213> Ehrlichia chaffeensis

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Ile Ser Gly Asn Phe Tyr Val Ser Gly Lys Tyr Met Pro Ser Ala Ser  
35 40 45

His Phe Gly Met Phe Ser Ala Lys Glu Glu Lys Asn Pro Thr Val Ala  
50 55 60

Leu Tyr Gly Leu Lys Gln Asp Trp Glu Gly Ile Ser Ser Ser Ser His  
65 70 75 80

Asn Asp Asn His Phe Asn Asn Lys Gly Tyr Ser Phe Lys Tyr Glu Asn  
85 90 95

Asn Pro Phe Leu Gly Phe Ala Gly Ala Ile Gly Tyr Ser Met Gly Gly  
 100 105 110

Pro Arg Val Glu Phe Glu Val Ser Tyr Glu Thr Phe Asp Val Lys Asn  
 115 120 125

Gln Gly Asn Asn Tyr Lys Asn Asp Ala His Arg Tyr Cys Ala Leu Gly  
 130 135 140

Gln Gln Asp Asn Ser Gly Ile Pro Lys Thr Ser Lys Tyr Val Leu Leu  
 145 150 155 160

Lys Ser Glu Gly Leu Leu Asp Ile Ser Phe Met Leu Asn Ala Cys Tyr  
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Asp Ile Ile Asn Glu Ser Ile Pro Leu Ser Pro Tyr Ile Cys Ala Gly  
 180 185 190

Val Gly Thr Asp Leu Ile Ser Met Phe Glu Ala Thr Asn Pro Lys Ile  
 195 200 205

Ser Tyr Gln Gly Lys Leu Gly Leu Ser Tyr Ser Ile Asn Pro Glu Ala  
 210 215 220

Ser Val Phe Ile Gly Gly His Phe His Lys Val Ile Gly Asn Glu Phe  
 225 230 235 240

Arg Asp Ile Pro Thr Leu Lys Ala Phe Val Thr Ser Ser Ala Thr Pro  
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Asp Leu Ala Ile Val Thr Leu Ser Val Cys His Phe Gly Ile Glu Leu  
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Gly Gly Arg Phe Asn Phe  
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<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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 gtttctaatt tagattttgt tccaaaagca agatggccgt tagaaagcat aaaaaggctc 3360



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 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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 <223> Complement to SEQ ID NO:2, nucleotides <1..372  
 Hypothetical dimethyl adenosine transferase  
 Product="lhworfli"

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 tttaccttga aattctttta taattttatc atgtattggt aataatctac tgtctttctc 180

tatagatatt aatTTTTtag gattctTTTT gagtattgaa taagtcattg taccaagtcc 240  
 gggaccaatt tcaataattg aaaaattgct aatgtttcct gcataattaa ctattttatc 300  
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 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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 Hypothetical triosephosphate isomerase  
 Product="lhworf2"

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 1 5 10 15  
 act ttt tct tcg ttt aca aag gag ctt agt aac cgt tta att aat ata 96  
 Thr Phe Ser Ser Phe Thr Lys Glu Leu Ser Asn Arg Leu Ile Asn Ile  
 20 25 30  
 gaa gat aaa gta aag gta gta tta tgc cca cca ttt att gcg tta tct 144  
 Glu Asp Lys Val Lys Val Val Leu Cys Pro Pro Phe Ile Ala Leu Ser  
 35 40 45  
 act tat gtt aat tgt cca cat aat att aag ttt ggt gga cag aac tgt 192  
 Thr Tyr Val Asn Cys Pro His Asn Ile Lys Phe Gly Gly Gln Asn Cys  
 50 55 60  
 tgt tat gta tct agt ggg aag tac act gga gaa att agt gct agt atg 240  
 Cys Tyr Val Ser Ser Gly Lys Tyr Thr Gly Glu Ile Ser Ala Ser Met  
 65 70 75 80  
 tta tat aac tct gga tgt agt tat gta ata gtg ggt cac tct gaa agg 288  
 Leu Tyr Asn Ser Gly Cys Ser Tyr Val Ile Val Gly His Ser Glu Arg  
 85 90 95  
 agg agt acg ttt cat gaa act gat cat gat gtt agg tta aaa gct gaa 336  
 Arg Ser Thr Phe His Glu Thr Asp His Asp Val Arg Leu Lys Ala Glu  
 100 105 110  
 tgt gcg atc gaa tca gga tta ata cca att att tgt gtt gga gaa act 384  
 Cys Ala Ile Glu Ser Gly Leu Ile Pro Ile Ile Cys Val Gly Glu Thr  
 115 120 125

tta cta gat agg gaa aat ggt atg cta aaa gat act tta tta agt caa 432  
 Leu Leu Asp Arg Glu Asn Gly Met Leu Lys Asp Thr Leu Leu Ser Gln  
 130 135 140

tgt agt gaa tct ttt cct aaa aat ggt aag ttt atc ata gca tat gag 480  
 Cys Ser Glu Ser Phe Pro Lys Asn Gly Lys Phe Ile Ile Ala Tyr Glu  
 145 150 155 160

cca gta tgg gca ata ggg aac aat aaa ata cct tct act gat gta ata 528  
 Pro Val Trp Ala Ile Gly Asn Asn Lys Ile Pro Ser Thr Asp Val Ile  
 165 170 175

ata gaa gct tta gag att att agg tca tat gat tat gta tct gat atc 576  
 Ile Glu Ala Leu Glu Ile Ile Arg Ser Tyr Asp Tyr Val Ser Asp Ile  
 180 185 190

ata tat ggt gga gca gta aat cat act aat gta ggt gat att gta agt 624  
 Ile Tyr Gly Gly Ala Val Asn His Thr Asn Val Gly Asp Ile Val Ser  
 195 200 205

atc aat caa ttg tct ggt gtt tta gtt ggt agt gct agt tta gat atg 672  
 Ile Asn Gln Leu Ser Gly Val Leu Val Gly Ser Ala Ser Leu Asp Met  
 210 215 220

gag agt ttt ttt aat ata ata tgt agt gct ata aat gtg agg caa agt 720  
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 225 230 235 240

taa 723

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 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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 20 25 30

Glu Asp Lys Val Lys Val Val Leu Cys Pro Pro Phe Ile Ala Leu Ser  
 35 40 45

Thr Tyr Val Asn Cys Pro His Asn Ile Lys Phe Gly Gly Gln Asn Cys  
 50 55 60

Cys Tyr Val Ser Ser Gly Lys Tyr Thr Gly Glu Ile Ser Ala Ser Met  
65 70 75 80

Leu Tyr Asn Ser Gly Cys Ser Tyr Val Ile Val Gly His Ser Glu Arg  
85 90 95

Arg Ser Thr Phe His Glu Thr Asp His Asp Val Arg Leu Lys Ala Glu  
100 105 110

Cys Ala Ile Glu Ser Gly Leu Ile Pro Ile Ile Cys Val Gly Glu Thr  
115 120 125

Leu Leu Asp Arg Glu Asn Gly Met Leu Lys Asp Thr Leu Leu Ser Gln  
130 135 140

Cys Ser Glu Ser Phe Pro Lys Asn Gly Lys Phe Ile Ile Ala Tyr Glu  
145 150 155 160

Pro Val Trp Ala Ile Gly Asn Asn Lys Ile Pro Ser Thr Asp Val Ile  
165 170 175

Ile Glu Ala Leu Glu Ile Ile Arg Ser Tyr Asp Tyr Val Ser Asp Ile  
180 185 190

Ile Tyr Gly Gly Ala Val Asn His Thr Asn Val Gly Asp Ile Val Ser  
195 200 205

Ile Asn Gln Leu Ser Gly Val Leu Val Gly Ser Ala Ser Leu Asp Met  
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Glu Ser Phe Phe Asn Ile Ile Cys Ser Ala Ile Asn Val Arg Gln Ser  
225 230 235 240

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<223> Corresponds to SEQ ID NO:2, nucleotides 1333..2313  
Hypothetical cell surface protein precursor  
Product="lhworf3"

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aat gct gcc att gct tca act gac tca tca gaa gat aaa cag tat att	96
Asn Ala Ala Ile Ala Ser Thr Asp Ser Ser Glu Asp Lys Gln Tyr Ile	
20 25 30	
tta att ggt act ggt tct atg act gga gta tat tat cct ata gga ggt	144
Leu Ile Gly Thr Gly Ser Met Thr Gly Val Tyr Tyr Pro Ile Gly Gly	
35 40 45	
agc ata tgt agg ttt att gca tct gat tat ggt aat gat aat aac agc	192
Ser Ile Cys Arg Phe Ile Ala Ser Asp Tyr Gly Asn Asp Asn Asn Ser	
50 55 60	
ata gtt tgt tct ata tct tct aca act ggt agc gta tat aat ctt aat	240
Ile Val Cys Ser Ile Ser Ser Thr Thr Gly Ser Val Tyr Asn Leu Asn	
65 70 75 80	
tct atg cgt tat gca aat atg gat ata ggt att att caa tct gat tta	288
Ser Met Arg Tyr Ala Asn Met Asp Ile Gly Ile Ile Gln Ser Asp Leu	
85 90 95	
gag tac tat gca tat aat ggt att ggt tta tat gaa aaa atg cca gca	336
Glu Tyr Tyr Ala Tyr Asn Gly Ile Gly Leu Tyr Glu Lys Met Pro Ala	
100 105 110	
atg agg cat cta aga ata tta tct tca tta cat aaa gaa tat ctt aca	384
Met Arg His Leu Arg Ile Leu Ser Ser Leu His Lys Glu Tyr Leu Thr	
115 120 125	
att gtt gtt agg gcg aat tct aat ata tca gtt att gat gat ata aaa	432
Ile Val Val Arg Ala Asn Ser Asn Ile Ser Val Ile Asp Asp Ile Lys	
130 135 140	
ggc aaa aga gtt aat att ggt agt cct ggt act ggt gta aga ata gca	480
Gly Lys Arg Val Asn Ile Gly Ser Pro Gly Thr Gly Val Arg Ile Ala	
145 150 155 160	
atg tta aaa ttg tta aat gaa aaa gga tgg gga aga aaa gat ttt gct	528
Met Leu Lys Leu Leu Asn Glu Lys Gly Trp Gly Arg Lys Asp Phe Ala	
165 170 175	
gtt atg gca gaa tta aaa tca tca gag caa gct caa gca tta tgt gat	576
Val Met Ala Glu Leu Lys Ser Ser Glu Gln Ala Gln Ala Leu Cys Asp	
180 185 190	
aat aaa att gat gtg atg gta gat gtt gtt gga cat cct aat gct gca	624
Asn Lys Ile Asp Val Met Val Asp Val Val Gly His Pro Asn Ala Ala	
195 200 205	

att caa gaa gca gca gca act tgt gat ata aaa ttt att tct tta gat 672  
 Ile Gln Glu Ala Ala Ala Thr Cys Asp Ile Lys Phe Ile Ser Leu Asp  
 210 215 220

gat gat ctc ata gat aaa tta cat act aag tat ccc tat tat aaa agg 720  
 Asp Asp Leu Ile Asp Lys Leu His Thr Lys Tyr Pro Tyr Tyr Lys Arg  
 225 230 235 240

gat att att agt ggt gcg tta tac agt aac tta cct gat ata caa act 768  
 Asp Ile Ile Ser Gly Ala Leu Tyr Ser Asn Leu Pro Asp Ile Gln Thr  
 245 250 255

gtt tca gta aaa gct tct tta ata aca act act gaa tta agc aat gag 816  
 Val Ser Val Lys Ala Ser Leu Ile Thr Thr Thr Glu Leu Ser Asn Glu  
 260 265 270

ttg gcc tat aaa gtt gtt aaa tct ttg gtt agc cat tta cat gaa cta 864  
 Leu Ala Tyr Lys Val Val Lys Ser Leu Val Ser His Leu His Glu Leu  
 275 280 285

cat gga att act gga gct ctt aga aat ctt act gta aaa gac atg gta 912  
 His Gly Ile Thr Gly Ala Leu Arg Asn Leu Thr Val Lys Asp Met Val  
 290 295 300

cag tca gat att aca cct tta cat gac ggt gca aaa cgt tat tat aag 960  
 Gln Ser Asp Ile Thr Pro Leu His Asp Gly Ala Lys Arg Tyr Tyr Lys  
 305 310 315 320

gaa att gga gtt ata aaa taa 981  
 Glu Ile Gly Val Ile Lys  
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<210> 7  
 <211> 326  
 <212> PRT  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)  
 <400> 7

Met Lys Lys Ile Leu Val Thr Phe Leu Val Val Val Asn Val Phe Cys  
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Leu Ile Gly Thr Gly Ser Met Thr Gly Val Tyr Tyr Pro Ile Gly Gly  
 35 40 45

Ser Ile Cys Arg Phe Ile Ala Ser Asp Tyr Gly Asn Asp Asn Asn Ser  
 50 55 60

Ile Val Cys Ser Ile Ser Ser Thr Thr Gly Ser Val Tyr Asn Leu Asn  
65 70 75 80

Ser Met Arg Tyr Ala Asn Met Asp Ile Gly Ile Ile Gln Ser Asp Leu  
85 90 95

Glu Tyr Tyr Ala Tyr Asn Gly Ile Gly Leu Tyr Glu Lys Met Pro Ala  
100 105 110

Met Arg His Leu Arg Ile Leu Ser Ser Leu His Lys Glu Tyr Leu Thr  
115 120 125

Ile Val Val Arg Ala Asn Ser Asn Ile Ser Val Ile Asp Asp Ile Lys  
130 135 140

Gly Lys Arg Val Asn Ile Gly Ser Pro Gly Thr Gly Val Arg Ile Ala  
145 150 155 160

Met Leu Lys Leu Leu Asn Glu Lys Gly Trp Gly Arg Lys Asp Phe Ala  
165 170 175

Val Met Ala Glu Leu Lys Ser Ser Glu Gln Ala Gln Ala Leu Cys Asp  
180 185 190

Asn Lys Ile Asp Val Met Val Asp Val Val Gly His Pro Asn Ala Ala  
195 200 205

Ile Gln Glu Ala Ala Ala Thr Cys Asp Ile Lys Phe Ile Ser Leu Asp  
210 215 220

Asp Asp Leu Ile Asp Lys Leu His Thr Lys Tyr Pro Tyr Tyr Lys Arg  
225 230 235 240

Asp Ile Ile Ser Gly Ala Leu Tyr Ser Asn Leu Pro Asp Ile Gln Thr  
245 250 255

Val Ser Val Lys Ala Ser Leu Ile Thr Thr Thr Glu Leu Ser Asn Glu  
260 265 270

Leu Ala Tyr Lys Val Val Lys Ser Leu Val Ser His Leu His Glu Leu  
275 280 285

His Gly Ile Thr Gly Ala Leu Arg Asn Leu Thr Val Lys Asp Met Val  
 290 295 300

Gln Ser Asp Ile Thr Pro Leu His Asp Gly Ala Lys Arg Tyr Tyr Lys  
 305 310 315 320

Glu Ile Gly Val Ile Lys  
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<210> 8  
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 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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 <222> (1)..(756)  
 <223> Corresponds to SEQ ID NO:2, nucleotides 2611..3366  
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 Product="lhworf4"

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 gtt aat cat ctg gaa gca cat act ttg cta ata cga atg ttt cat gat 96  
 Val Asn His Leu Glu Ala His Thr Leu Ile Arg Met Phe His Asp  
 20 25 30  
 att gat ttt cca ttt tta gta ttg atc ata tct ggc gga cat tgt cag 144  
 Ile Asp Phe Pro Phe Leu Val Leu Ile Ile Ser Gly Gly His Cys Gln  
 35 40 45  
 ttt tta ata gtt cat gat gtt gga tgt tat caa aga tta ggt tct tct 192  
 Phe Leu Ile Val His Asp Val Gly Cys Tyr Gln Arg Leu Gly Ser Ser  
 50 55 60  
 tta gat gac tcc ctt ggt gaa gta ttt gat aaa gta gca aga atg ttg 240  
 Leu Asp Asp Ser Leu Gly Glu Val Phe Asp Lys Val Ala Arg Met Leu  
 65 70 75 80  
 aat ttg gga tat cct gga ggg cca att att gaa aaa aaa tcc ata atg 288  
 Asn Leu Gly Tyr Pro Gly Gly Pro Ile Ile Glu Lys Lys Ser Ile Met  
 85 90 95  
 ggt gat agc aaa agt ttt ttt cta cca cgt gca tta atc aat cgt ctt 336  
 Gly Asp Ser Lys Ser Phe Phe Leu Pro Arg Ala Leu Ile Asn Arg Leu  
 100 105 110



gga tgt gat ttt tct ttc tcc ggt att aag acg gca gta aga aat att 384  
 Gly Cys Asp Phe Ser Phe Ser Gly Ile Lys Thr Ala Val Arg Asn Ile  
           115                                  120                                  125

gtt gta aat caa aaa tat ata gat aat gat ttt ata tgt aat att tca 432  
 Val Val Asn Gln Lys Tyr Ile Asp Asn Asp Phe Ile Cys Asn Ile Ser  
           130                                  135                                  140

gct tct ttt caa gat tgt att ggt gat ata tta gta aac agg att act 480  
 Ala Ser Phe Gln Asp Cys Ile Gly Asp Ile Leu Val Asn Arg Ile Thr  
           145                                  150                                  155                                  160

aat gct att cat atg tca caa gct ata aat tgt aag att aat aag tta 528  
 Asn Ala Ile His Met Ser Gln Ala Ile Asn Cys Lys Ile Asn Lys Leu  
                                   165                                  170                                  175

gta gta act gga ggt gtt gca gct aat cac cta tta cgt aat cgt ata 576  
 Val Val Thr Gly Gly Val Ala Ala Asn His Leu Leu Arg Asn Arg Ile  
                                   180                                  185                                  190

tca att tgt gta aaa gat aat aat ttt gag gtg cta tat cct cca act 624  
 Ser Ile Cys Val Lys Asp Asn Asn Phe Glu Val Leu Tyr Pro Pro Thr  
                                   195                                  200                                  205

gag tta tgt act gat aat gga att atg gtt ggg tgg gct ggt att gaa 672  
 Glu Leu Cys Thr Asp Asn Gly Ile Met Val Gly Trp Ala Gly Ile Glu  
           210                                  215                                  220

aat tta tct aaa ggt tat gtt tct aat tta gat ttt gtt cca aaa gca 720  
 Asn Leu Ser Lys Gly Tyr Val Ser Asn Leu Asp Phe Val Pro Lys Ala  
           225                                  230                                  235                                  240

aga tgg ccg tta gaa agc ata aaa agg tct agt taa 756  
 Arg Trp Pro Leu Glu Ser Ile Lys Arg Ser Ser  
                                   245                                  250

<210> 9  
 <211> 251  
 <212> PRT  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 9

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Val Asn His Leu Glu Ala His Thr Leu Leu Ile Arg Met Phe His Asp  
           20                                  25                                  30

Ile Asp Phe Pro Phe Leu Val Leu Ile Ile Ser Gly Gly His Cys Gln  
           35                                  40                                  45

Arg Trp Pro Leu Glu Ser Ile Lys Arg Ser Ser  
245 250

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<211> 222  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
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 <223> Corresponds to SEQ ID NO:2, nucleotides 4065..4286  
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<400> 10  
 atg act ctt ttt tac tat aga aaa ttc acc aat cta aca ata gta aat 48  
 Met Thr Leu Phe Tyr Tyr Arg Lys Phe Thr Asn Leu Thr Ile Val Asn  
 1 5 10 15  
 aaa aat ttt tta att tat atg aca ttt gta tat tac tat aaa tca gta 96  
 Lys Asn Phe Leu Ile Tyr Met Thr Phe Val Tyr Tyr Tyr Lys Ser Val  
 20 25 30  
 ttt att aaa gtt aag aat att aat aat gta ttt aag ttt aaa aaa aac 144  
 Phe Ile Lys Val Lys Asn Ile Asn Asn Val Phe Lys Phe Lys Lys Asn  
 35 40 45  
 ttt ttt gta aat agt cat att aat ata act ttt agc aat ata aat att 192  
 Phe Phe Val Asn Ser His Ile Asn Ile Thr Phe Ser Asn Ile Asn Ile  
 50 55 60  
 gaa ttt tca gta ctt acg tca tac tgt taa 222  
 Glu Phe Ser Val Leu Thr Ser Tyr Cys  
 65 70

<210> 11  
 <211> 73  
 <212> PRT  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 11  
 Met Thr Leu Phe Tyr Tyr Arg Lys Phe Thr Asn Leu Thr Ile Val Asn  
 1 5 10 15  
 Lys Asn Phe Leu Ile Tyr Met Thr Phe Val Tyr Tyr Tyr Lys Ser Val  
 20 25 30  
 Phe Ile Lys Val Lys Asn Ile Asn Asn Val Phe Lys Phe Lys Lys Asn  
 35 40 45  
 Phe Phe Val Asn Ser His Ile Asn Ile Thr Phe Ser Asn Ile Asn Ile  
 50 55 60

Glu Phe Ser Val Leu Thr Ser Tyr Cys  
65 70

<210> 12  
<211> 4913  
<212> DNA  
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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atatagattt gtagtaacta ctatgtaaag tgcattttat ataattttta ataaataaat 180  
aaaaaaggta agattatgaa tatattcaat tatatgcaga taatgcctaa tataagtgtt 240  
gatgcatttg ttgcacctac tgctgtaatt ataggtgatg tttgtgtaaa tgacaagtgt 300  
agcatttggt ataactcagt attacgtgga gatgtaggcc aaattgttat tgggtgtaggt 360  
actaatattc aagatgggac aataatacat gttgatagga aatatggtaa tacgaatatt 420  
ggcaaaaagg ttactattgg gcattgggtg atattacatg cttgtgagat acaagattat 480  
gtgcttggtg gaatgggac tattattatg gataacgttg tgggtgaaaa gaatgcaatg 540  
gtggctgctg gatcattagt ggtaagaggt aaagttgtga aaactgggtga attatgggct 600  
ggtaggcctg cacaattttt aagaatgttg tctagtgatg aaattaaaga gataagtaaa 660  
tctgctgata actatataga gcttgccagt gattacataa ctggtaagtt gtaatttttag 720  
ttacgctcaa aagataatta tctgtattga ttgagaattt actagtgttt ttttatttta 780  
tatgaatcta tgctatggat gactctatat tctatgtttc aattaattac tagatgtagc 840  
ctaggaagta gggttttgta ttatttcatt attattgttt taaactatgt tagtaatatc 900  
tgtaaaatgg gtagattact tatgtagtat agattttaat taacaattaa agttaaatc 960  
ctttaatgtg tgtaattct ggtgaatact tttattcaag tattttaatt acttagtata 1020  
ttcttgatgg tgtggtttgt tgaaaattac ttttctgtta taggatggag aataaattca 1080  
tgtagttat gattggtgaa attagtgatg tataaattat aaatcaaagtg tgctaatttg 1140  
ttgacaatgg gaatttctat gatttatgct atggattata catcatatga tggtgggttt 1200  
gtatgtaatt tatagtaaat aagtagtttt ttttattata tttcatatgt cattttttgt 1260  
gttgagtgtg gtctaaggaa tttttgtggt tgcatttatg agtgaagtac aagtaagggc 1320

tgaaaatctt ggtggtgagt caatattaga agctccaatt cgagtttctg ttaagattgg 1380  
 tgatagtatt aagcaagggtg atgtattggt tatcattgaa acggataaaa cttctctaga 1440  
 aattgtatct cctgtagatg gaacagttag taaagtattt atagcagatg aagaaattat 1500  
 agaacgtgat caacttttat gtacaataaa tgttggtgaa ttatcacata ttgtccagtc 1560  
 tcaaactcag gatcctaaaa cagataatgg tgatattatt aatgatgata ttcagacggt 1620  
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 cattaatggt gtttcaaaag atcatagtgt gctttctgaa caatgtagta ttacttctca 1800  
 tgagaagaga gaagaacgtg ttaagatgag taaaattagg cagggtgattg ctgcgaggct 1860  
 taaggagtct caaaatactg ctgcaatatt aactacgttt aatgaagtgg atatgaagaa 1920  
 tgttatggat cttcgtgttc agtataggga gacctttgaa aagaaatatg gtgtcaaaact 1980  
 tggatttatg tcttttttta taaaagcggg agtattagca ttaaaagaat taccagtaat 2040  
 taatgctgag atatctggta atgagattat atataaacat tattatgaca taggtattgc 2100  
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 catttcacaa tcatagcagt aattgtttta catcttgagt ttctgtatat ttacgaagt 2580  
 aatgtacaag gttgctgtct gacaatatta agtttttagtg ggttttgttt attggtttat 2640  
 tgtaagtaa ttatagtaaa gtataataaa tgtaatacag ttatagtgtc gatatagcta 2700  
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 agtgtaaatt attttatggt gttatataaa aacgatctca aaaagtatta atttatataa 2820  
 aaataaaatc taaatttttag atggctttat tgcaatgtct tttatgttgt tatatgagtt 2880  
 aatgttaaat taaaaagtta tgttatagta taaaaataaa tgtaacattt ctttagctat 2940  
 gcgaaatata taaaactttc tttatcactg tgatgttttt gtagagctat ctatgaacat 3000

attgaaatgt taacattatt gaatgttttt cttgtaatta tacgttaatg tataggttat 3060  
 ttggtaaaag gtatgagcta aatcttgtgt taatataaaa aattaaattg tacggtaatg 3120  
 taaattttatt aagctacatc ttttctgtaa aaaatttttg tatttctgtc atctgatgta 3180  
 taaggttaca aatgcagaaa tgtaaagtag tttatatgta tgaaggctat ggtagcctat 3240  
 ataagattgc ctacacatat tataattatc tattgatact tttagtagta ctaatatgat 3300  
 aagaatatga ctaaattttt ttattgcata taaaaagtag cagtagttgt tgtagagtaa 3360  
 tgtagctttt tgaatgatat cttataaatt aataatatta gtacaatatt tttataatat 3420  
 ttaagaaatt aaagaatcaa aatttaaagt tattatatct taattatcta aattttgttg 3480  
 ataggtaatc ctattttttg aataagaagt gtgtagttta tgattaacaa aacattgttg 3540  
 atgtatttcg taatagtata ttaacagaat ttttgtatgt ttatttttta gaatttaata 3600  
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 ataagggtgtg ttagcgggtg tttgtatggt gttgagtaaa gataaaaata aaaagaaaaa 3720  
 agatcccaat aatcaagaaa atgatgaaag gaatcaaact ggtgaatcag gtgttaaacc 3780  
 tgaagtacca aaccagcaaa gtattcaaga tataggtcag ggtgtagtag aaggggcaac 3840  
 agatgctagt gatatgagt gtgttggaag atgtgctttt tctgtgacta tagagattga 3900  
 atcatcttca tcaacatctc agccaagtag tagtcttgaa aatatatata tgaggcaggg 3960  
 tgctaggcca aaaactagga ctcaaagtaa agttgcacag cagagtacag gacaatttca 4020  
 gagtataggg tcacagagta gtttgccctc tgtatttgta aaacgtatgg ctgatgtatc 4080  
 tttggaaaag gcagaatgtg atacatatat atgtgggact aaaaggcgta gcgatcaaag 4140  
 cacaaggtca agggaggact taccttctag gtttgcaaaa tgtgcatctg atatatTTTT 4200  
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 atctgatgtc gtatataaaa aatgtgtatc cttacaacaa aaatgtggca gtttttagaca 4380  
 gtttagtaat tcttgtctag caagattaag aggtatgcat atgggatatc ttaatttttt 4440  
 tatgaaacga ttgtttatgg ctcaaggtaa cacattagtt atgctgtggg agtacttgca 4500  
 gatgttatca aatatcacta aacattctga cgaggctgtt gttcttgtga agttaaatct 4560  
 tatgtcacia tatttgcttg catttggtgc gtatcaggta agccggtcaa tgtaaacaca 4620

gaagcttagt aattctgatt tttatgcaat tgatattttg ttattagaat taatattggt 4680  
 ttcgtacaag gagagagtga atctttattg tgctcaaaga gaagttctta ggatgtatgc 4740  
 tataatggat tataattctg gttataatcc taattgtagt aatataaagt tttgttatgt 4800  
 aatggtgcaa ttattccgtg atttattatc tgcaagacaa agtatggtgt taggtgattt 4860  
 agatttaciaa ttagttaatt tattgattat cagtgttagt attcaaatag atc 4913

<210> 13  
 <211> 519  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
 <221> CDS  
 <222> (1)..(519)  
 <223> Corresponds to SEQ ID NO:12, nucleotides 196..714  
 Hypothetical ferripyochelin binding protein  
 Product="4hworf1"

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 atg aat ata ttc aat tat atg cag ata atg cct aat ata agt gtt gat 48  
 Met Asn Ile Phe Asn Tyr Met Gln Ile Met Pro Asn Ile Ser Val Asp  
 1 5 10 15  
 gca ttt gtt gca cct act gct gta att ata ggt gat gtt tgt gta aat 96  
 Ala Phe Val Ala Pro Thr Ala Val Ile Ile Gly Asp Val Cys Val Asn  
 20 25 30  
 gac aag tgt agc att tgg tat aac tca gta tta cgt gga gat gta ggc 144  
 Asp Lys Cys Ser Ile Trp Tyr Asn Ser Val Leu Arg Gly Asp Val Gly  
 35 40 45  
 caa att gtt att ggt gta ggt act aat att caa gat ggg aca ata ata 192  
 Gln Ile Val Ile Gly Val Gly Thr Asn Ile Gln Asp Gly Thr Ile Ile  
 50 55 60  
 cat gtt gat agg aaa tat ggt aat acg aat att ggc aaa aag gtt act 240  
 His Val Asp Arg Lys Tyr Gly Asn Thr Asn Ile Gly Lys Lys Val Thr  
 65 70 75 80  
 att ggg cat ggg tgt ata tta cat gct tgt gag ata caa gat tat gtg 288  
 Ile Gly His Gly Cys Ile Leu His Ala Cys Glu Ile Gln Asp Tyr Val  
 85 90 95  
 ctt gtt gga atg gga tct att att atg gat aac gtt gtg gtt gaa aag 336  
 Leu Val Gly Met Gly Ser Ile Ile Met Asp Asn Val Val Val Glu Lys  
 100 105 110  
 aat gca atg gtg gct gct gga tca tta gtg gta aga ggt aaa gtt gtg 384  
 Asn Ala Met Val Ala Ala Gly Ser Leu Val Val Arg Gly Lys Val Val

115	120	125	
aaa act ggt gaa tta tgg gct ggt agg cct gca caa ttt tta aga atg			432
Lys Thr Gly Glu Leu Trp Ala Gly Arg Pro Ala Gln Phe Leu Arg Met			
130	135	140	
ttg tct agt gat gaa att aaa gag ata agt aaa tct gct gat aac tat			480
Leu Ser Ser Asp Glu Ile Lys Glu Ile Ser Lys Ser Ala Asp Asn Tyr			
145	150	155	160
ata gag ctt gcc agt gat tac ata act ggt aag ttg taa			519
Ile Glu Leu Ala Ser Asp Tyr Ile Thr Gly Lys Leu			
165	170		

<210> 14  
 <211> 172  
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 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 14

Met Asn Ile Phe Asn Tyr Met Gln Ile Met Pro Asn Ile Ser Val Asp	
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Ala Phe Val Ala Pro Thr Ala Val Ile Ile Gly Asp Val Cys Val Asn	
20	30

Asp Lys Cys Ser Ile Trp Tyr Asn Ser Val Leu Arg Gly Asp Val Gly	
35	45

Gln Ile Val Ile Gly Val Gly Thr Asn Ile Gln Asp Gly Thr Ile Ile	
50	60

His Val Asp Arg Lys Tyr Gly Asn Thr Asn Ile Gly Lys Lys Val Thr	
65	80

Ile Gly His Gly Cys Ile Leu His Ala Cys Glu Ile Gln Asp Tyr Val	
85	95

Leu Val Gly Met Gly Ser Ile Ile Met Asp Asn Val Val Val Glu Lys	
100	110

Asn Ala Met Val Ala Ala Gly Ser Leu Val Val Arg Gly Lys Val Val	
115	125

Lys Thr Gly Glu Leu Trp Ala Gly Arg Pro Ala Gln Phe Leu Arg Met



130

135

140

Leu Ser Ser Asp Glu Ile Lys Glu Ile Ser Lys Ser Ala Asp Asn Tyr  
 145 150 155 160

Ile Glu Leu Ala Ser Asp Tyr Ile Thr Gly Lys Leu  
 165 170

<210> 15  
 <211> 1209  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)  
 <220>  
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 <223> Corresponds to SEQ ID NO:12, nucleotides 1298..2506  
 Hypothetical dihydrolipoamide acetyltransferase  
 Product="4hworf2"

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 1 5 10 15  
 tta gaa gct cca att cga gtt tct gtt aag att ggt gat agt att aag 96  
 Leu Glu Ala Pro Ile Arg Val Ser Val Lys Ile Gly Asp Ser Ile Lys  
 20 25 30  
 caa ggt gat gta ttg ttt atc att gaa acg gat aaa act tct cta gaa 144  
 Gln Gly Asp Val Leu Phe Ile Ile Glu Thr Asp Lys Thr Ser Leu Glu  
 35 40 45  
 att gta tct cct gta gat gga aca gtt agt aaa gta ttt ata gca gat 192  
 Ile Val Ser Pro Val Asp Gly Thr Val Ser Lys Val Phe Ile Ala Asp  
 50 55 60  
 gaa gaa att ata gaa cgt gat caa ctt tta tgt aca ata aat gtt ggt 240  
 Glu Glu Ile Ile Glu Arg Asp Gln Leu Leu Cys Thr Ile Asn Val Gly  
 65 70 75 80  
 gaa tta tca cat att gtc cag tct caa act cag gat cct aaa aca gat 288  
 Glu Leu Ser His Ile Val Gln Ser Gln Thr Gln Asp Pro Lys Thr Asp  
 85 90 95  
 aat ggt gat att att aat gat gat att cag acg ttt ata cag aaa aaa 336  
 Asn Gly Asp Ile Ile Asn Asp Asp Ile Gln Thr Phe Ile Gln Lys Lys  
 100 105 110  
 gat gct cct tct gca gta aaa att atg gca gaa aat tca att gat aag 384  
 Asp Ala Pro Ser Ala Val Lys Ile Met Ala Glu Asn Ser Ile Asp Lys

115	120	125	
aat cag atc aat ggg tct ggt att ggt gga aga att aca aaa tct gat			432
Asn Gln Ile Asn Gly Ser Gly Ile Gly Gly Arg Ile Thr Lys Ser Asp			
130	135	140	
ggt tta gac cac att aat gtt gtt tca aaa gat cat agt gtg ctt tct			480
Val Leu Asp His Ile Asn Val Val Ser Lys Asp His Ser Val Leu Ser			
145	150	155	160
gaa caa tgt agt att act tct cat gag aag aga gaa gaa cgt gtt aag			528
Glu Gln Cys Ser Ile Thr Ser His Glu Lys Arg Glu Glu Arg Val Lys			
165	170	175	
atg agt aaa att agg cag gtg att gct gcg agg ctt aag gag tct caa			576
Met Ser Lys Ile Arg Gln Val Ile Ala Ala Arg Leu Lys Glu Ser Gln			
180	185	190	
aat act gct gca ata tta act acg ttt aat gaa gtg gat atg aag aat			624
Asn Thr Ala Ala Ile Leu Thr Thr Phe Asn Glu Val Asp Met Lys Asn			
195	200	205	
ggt atg gat ctt cgt gtt cag tat agg gag acc ttt gaa aag aaa tat			672
Val Met Asp Leu Arg Val Gln Tyr Arg Glu Thr Phe Glu Lys Lys Tyr			
210	215	220	
ggt gtc aaa ctt gga ttt atg tct ttt ttt ata aaa gcg gta gta tta			720
Gly Val Lys Leu Gly Phe Met Ser Phe Phe Ile Lys Ala Val Val Leu			
225	230	235	240
gca tta aaa gaa tta cca gta att aat gct gag ata tct ggt aat gag			768
Ala Leu Lys Glu Leu Pro Val Ile Asn Ala Glu Ile Ser Gly Asn Glu			
245	250	255	
att ata tat aaa cat tat tat gac ata ggt att gct gta ggg aca gac			816
Ile Ile Tyr Lys His Tyr Tyr Asp Ile Gly Ile Ala Val Gly Thr Asp			
260	265	270	
aaa ggt cta gtt gtt cca gta atg cgt gat gct gat aag atg tct tgt			864
Lys Gly Leu Val Val Pro Val Met Arg Asp Ala Asp Lys Met Ser Cys			
275	280	285	
gct gag ctt gag tta acc tta gct tct tta ggt aag aaa gct agg gaa			912
Ala Glu Leu Glu Leu Thr Leu Ala Ser Leu Gly Lys Lys Ala Arg Glu			
290	295	300	
ggg aaa tta gaa gtt tca gat atg gct ggt gca act ttt act att act			960
Gly Lys Leu Glu Val Ser Asp Met Ala Gly Ala Thr Phe Thr Ile Thr			
305	310	315	320
aat ggt ggg gta tat ggt tca tta tta tct act cct ata att aat cct			1008
Asn Gly Gly Val Tyr Gly Ser Leu Leu Ser Thr Pro Ile Ile Asn Pro			
325	330	335	
cct cag tct ggt att tta ggt atg cac tct ata caa aaa cga cca gta			1056

Pro Gln Ser Gly Ile Leu Gly Met His Ser Ile Gln Lys Arg Pro Val  
 340 345 350

gta gtt aat gat aat tct ata gag att aga cct atg atg tac att gca 1104  
 Val Val Asn Asp Asn Ser Ile Glu Ile Arg Pro Met Met Tyr Ile Ala  
 355 360 365

tta tct tat gat cat aga att gtt gat gga caa ggt gct gta aca ttt 1152  
 Leu Ser Tyr Asp His Arg Ile Val Asp Gly Gln Gly Ala Val Thr Phe  
 370 375 380

tta gta aga gtt aaa cag tat att gaa gat cca agt aga atg ttt cta 1200  
 Leu Val Arg Val Lys Gln Tyr Ile Glu Asp Pro Ser Arg Met Phe Leu  
 385 390 395 400

gaa ata taa 1209  
 Glu Ile

<210> 16  
 <211> 402  
 <212> PRT  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 16

Met Ser Glu Val Gln Val Arg Ala Glu Asn Leu Gly Gly Glu Ser Ile  
 1 5 10 15

Leu Glu Ala Pro Ile Arg Val Ser Val Lys Ile Gly Asp Ser Ile Lys  
 20 25 30

Gln Gly Asp Val Leu Phe Ile Ile Glu Thr Asp Lys Thr Ser Leu Glu  
 35 40 45

Ile Val Ser Pro Val Asp Gly Thr Val Ser Lys Val Phe Ile Ala Asp  
 50 55 60

Glu Glu Ile Ile Glu Arg Asp Gln Leu Leu Cys Thr Ile Asn Val Gly  
 65 70 75 80

Glu Leu Ser His Ile Val Gln Ser Gln Thr Gln Asp Pro Lys Thr Asp  
 85 90 95

Asn Gly Asp Ile Ile Asn Asp Asp Ile Gln Thr Phe Ile Gln Lys Lys  
 100 105 110

Asp Ala Pro Ser Ala Val Lys Ile Met Ala Glu Asn Ser Ile Asp Lys  
 115 120 125

Asn Gln Ile Asn Gly Ser Gly Ile Gly Gly Arg Ile Thr Lys Ser Asp  
 130 135 140

Val Leu Asp His Ile Asn Val Val Ser Lys Asp His Ser Val Leu Ser  
 145 150 155 160

Glu Gln Cys Ser Ile Thr Ser His Glu Lys Arg Glu Glu Arg Val Lys  
 165 170 175

Met Ser Lys Ile Arg Gln Val Ile Ala Ala Arg Leu Lys Glu Ser Gln  
 180 185 190

Asn Thr Ala Ala Ile Leu Thr Thr Phe Asn Glu Val Asp Met Lys Asn  
 195 200 205

Val Met Asp Leu Arg Val Gln Tyr Arg Glu Thr Phe Glu Lys Lys Tyr  
 210 215 220

Gly Val Lys Leu Gly Phe Met Ser Phe Phe Ile Lys Ala Val Val Leu  
 225 230 235 240

Ala Leu Lys Glu Leu Pro Val Ile Asn Ala Glu Ile Ser Gly Asn Glu  
 245 250 255

Ile Ile Tyr Lys His Tyr Tyr Asp Ile Gly Ile Ala Val Gly Thr Asp  
 260 265 270

Lys Gly Leu Val Val Pro Val Met Arg Asp Ala Asp Lys Met Ser Cys  
 275 280 285

Ala Glu Leu Glu Leu Thr Leu Ala Ser Leu Gly Lys Lys Ala Arg Glu  
 290 295 300

Gly Lys Leu Glu Val Ser Asp Met Ala Gly Ala Thr Phe Thr Ile Thr  
 305 310 315 320

Asn Gly Gly Val Tyr Gly Ser Leu Leu Ser Thr Pro Ile Ile Asn Pro  
 325 330 335

Pro Gln Ser Gly Ile Leu Gly Met His Ser Ile Gln Lys Arg Pro Val  
 340 345 350

Val Val Asn Asp Asn Ser Ile Glu Ile Arg Pro Met Met Tyr Ile Ala  
 355 360 365

Leu Ser Tyr Asp His Arg Ile Val Asp Gly Gln Gly Ala Val Thr Phe  
 370 375 380

Leu Val Arg Val Lys Gln Tyr Ile Glu Asp Pro Ser Arg Met Phe Leu  
 385 390 395 400

Glu Ile

<210> 17  
 <211> 1227  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)  
 <220>  
 <221> CDS  
 <222> (1)..(1227)  
 <223> Corresponds to SEQ ID NO:12, nucleotides 3686...>4913  
 Product="4hworf3i"

<400> 17  
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 1 5 10 15  
 caa gaa aat gat gaa agg aat caa act ggt gaa tca ggt gtt aaa cct 96  
 Gln Glu Asn Asp Glu Arg Asn Gln Thr Gly Glu Ser Gly Val Lys Pro  
 20 25 30  
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 Phe Ser Val Thr Ile Glu Ile Glu Ser Ser Ser Ser Thr Ser Gln Pro  
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Ser	Ser	Ser	Leu	Glu	Asn	Ile	Tyr	Met	Arg	Gln	Gly	Ala	Arg	Pro	Lys		
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Ser	Ile	Gly	Ser	Gln	Ser	Ser	Leu	Pro	Pro	Val	Phe	Val	Lys	Arg	Met		
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Ala	Asp	Val	Ser	Leu	Glu	Lys	Ala	Glu	Cys	Asp	Thr	Tyr	Ile	Cys	Gly		
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Met	Leu	Ser	Asn	Ile	Thr	Lys	His	Ser	Asp	Glu	Ala	Val	Val	Leu	Val		
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Lys	Leu	Asn	Leu	Met	Ser	Gln	Tyr	Leu	Leu	Ala	Phe	Gly	Ala	Tyr	Gln		
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<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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Phe Ser Val Thr Ile Glu Ile Glu Ser Ser Ser Ser Thr Ser Gln Pro  
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Ser Ser Ser Leu Glu Asn Ile Tyr Met Arg Gln Gly Ala Arg Pro Lys  
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Thr Arg Thr Gln Ser Lys Val Ala Gln Gln Ser Thr Gly Gln Phe Gln  
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Ser Ile Gly Ser Gln Ser Ser Leu Pro Pro Val Phe Val Lys Arg Met  
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Ala Asp Val Ser Leu Glu Lys Ala Glu Cys Asp Thr Tyr Ile Cys Gly  
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Thr Lys Arg Arg Ser Asp Gln Ser Thr Arg Ser Arg Glu Asp Leu Pro  
145 150 155 160

Ser Arg Phe Ala Lys Cys Ala Ser Asp Ile Phe Leu Thr Lys Pro Gln  
165 170 175

Asn Asn Asp Leu Asp Ile His Asp Thr Asp Lys Glu Lys Leu Ile His  
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Ser Leu Glu Glu Leu Asp Val Ala Leu Pro Thr Glu Ser Gly Gly Asp  
195 200 205

His Asn Val Leu Ser Asp Val Val Tyr Lys Lys Cys Val Ser Leu Gln  
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Gln Lys Cys Gly Ser Phe Arg Gln Phe Ser Asn Ser Cys Leu Ala Arg  
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Leu Arg Gly Met His Met Gly Tyr Leu Asn Phe Phe Met Lys Arg Leu  
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Phe Met Ala Gln Gly Asn Thr Leu Val Met Arg Gly Glu Tyr Leu Gln  
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Lys Leu Asn Leu Met Ser Gln Tyr Leu Leu Ala Phe Gly Ala Tyr Gln  
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Val Ser Arg Ser Met Leu Thr Gln Lys Leu Ser Asn Ser Asp Phe Tyr  
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Ala Ile Asp Ile Leu Leu Leu Glu Leu Ile Leu Val Ser Tyr Lys Glu  
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Phe Cys Tyr Val Met Val Gln Leu Phe Arg Asp Leu Leu Ser Ala Arg  
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Tyr Lys Asn Ser Val His Ser Phe Leu Ala Gln Ser Thr Ile Ile Asp  
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Ala Val Thr Leu Phe Lys Glu Thr Leu Glu Glu Lys Phe Cys Lys Gly	
210 215 220	
tta aaa aat aaa ata ttt ttt aat tat gca caa tat tta aaa agt cta	720
Leu Lys Asn Lys Ile Phe Phe Asn Tyr Ala Gln Tyr Leu Lys Ser Leu	
225 230 235 240	
ttt act atc gta aca tca aat cca aaa gta gac tat acc ctt cca caa	768
Phe Thr Ile Val Thr Ser Asn Pro Lys Val Asp Tyr Thr Leu Pro Gln	
245 250 255	
aat ata tat aga tat tgt gaa aca aga aga atg gta att tca aaa ata	816
Asn Ile Tyr Arg Tyr Cys Glu Thr Arg Arg Met Val Ile Ser Lys Ile	
260 265 270	
aca cat gat ata att cct ata tca gat cca gga act gat ata cgt att	864
Thr His Asp Ile Ile Pro Ile Ser Asp Pro Gly Thr Asp Ile Arg Ile	
275 280 285	
tat tgt gat ata cca gag tat gta acc gta tta tca gaa aca agt aac	912
Tyr Cys Asp Ile Pro Glu Tyr Val Thr Val Leu Ser Glu Thr Ser Asn	
290 295 300	
att act ata tac ggg aaa gaa gta ctt ggt aaa gtt tat agc ata tat	960
Ile Thr Ile Tyr Gly Lys Glu Val Leu Gly Lys Val Tyr Ser Ile Tyr	

305	310	315	320	
ggt aca att ata att aaa aac aat atg cca cat aat gaa cga gaa ata				1008
Gly Thr Ile Ile Ile Lys Asn Asn Met Pro His Asn Glu Arg Glu Ile				
	325	330	335	
agc tct cgt ata tgt tct tta ttt ggt cgt gtt ata atc aat gga aga				1056
Ser Ser Arg Ile Cys Ser Leu Phe Gly Arg Val Ile Ile Asn Gly Arg				
	340	345	350	
ata ctt aat cgg aaa cat aca ata cct agt ata ttt gaa att aac aac				1104
Ile Leu Asn Arg Lys His Thr Ile Pro Ser Ile Phe Glu Ile Asn Asn				
	355	360	365	
cat aac aca tac tta tca ctt aaa tat aat tct ata tta aca aaa ata				1152
His Asn Thr Tyr Leu Ser Leu Lys Tyr Asn Ser Ile Leu Thr Lys Ile				
	370	375	380	
aca agc agc tct gta ggt tcc gta aat gaa gaa aaa aaa tca caa atc				1200
Thr Ser Ser Ser Val Gly Ser Val Asn Glu Glu Lys Lys Ser Gln Ile				
	385	390	395	400
ttt gaa atc agt agg gat aca att ttg aat tca aca aat tat cag aga				1248
Phe Glu Ile Ser Arg Asp Thr Ile Leu Asn Ser Thr Asn Tyr Gln Arg				
	405	410	415	
aat ata tca aat tta aaa ata gaa cta cat aac cca gat gaa caa ctc				1296
Asn Ile Ser Asn Leu Lys Ile Glu Leu His Asn Pro Asp Glu Gln Leu				
	420	425	430	
aca gct act gtc ata tca tta gat tta aaa gat cat cca tta cct att				1344
Thr Ala Thr Val Ile Ser Leu Asp Leu Lys Asp His Pro Leu Pro Ile				
	435	440	445	
act aat aat aat act ata cct aat ata tta agc cta aca gac aat cac				1392
Thr Asn Asn Asn Thr Ile Pro Asn Ile Leu Ser Leu Thr Asp Asn His				
	450	455	460	
gca aca gat tca gaa tta cca agt gag ttt ttt agt aac aat gtt aac				1440
Ala Thr Asp Ser Glu Leu Pro Ser Glu Phe Phe Ser Asn Asn Val Asn				
	465	470	475	480
cca aaa agt gct gga att acg aga ata aaa aat aca att att att gag				1488
Pro Lys Ser Ala Gly Ile Thr Arg Ile Lys Asn Thr Ile Ile Ile Glu				
	485	490	495	
aaa tta act cct aca ata gga aga tat atg aat gtt gcc aca aaa aat				1536
Lys Leu Thr Pro Thr Ile Gly Arg Tyr Met Asn Val Ala Thr Lys Asn				
	500	505	510	
gga aca gta tta gat aaa tat ggg atc aca gaa gta att att caa agt				1584
Gly Thr Val Leu Asp Lys Tyr Gly Ile Thr Glu Val Ile Ile Gln Ser				
	515	520	525	
acc aga aac ttt gta ata tta tta cta cat gat gca aat gtt act ata				1632



Thr Arg Asn Phe Val Ile Leu Leu Leu His Asp Ala Asn Val Thr Ile  
 530 535 540

gaa tgt cca ttt tct gga gaa ata ttt aca aat aca ggt aat att aca 1680  
 Glu Cys Pro Phe Ser Gly Glu Ile Phe Thr Asn Thr Gly Asn Ile Thr  
 545 550 555 560

gtt att ggc cca gta act cac aat tct aaa ctt att tca aac ttt ggt 1728  
 Val Ile Gly Pro Val Thr His Asn Ser Lys Leu Ile Ser Asn Phe Gly  
 565 570 575

tca gtt tat gtt ggt aat ata tct cat cgg tca aat gca tta gca ata 1776  
 Ser Val Tyr Val Gly Asn Ile Ser His Arg Ser Asn Ala Leu Ala Ile  
 580 585 590

gat aac agc cgt att gta tct tca ctt ggg cat gtc aca att tat ggc 1824  
 Asp Asn Ser Arg Ile Val Ser Ser Leu Gly His Val Thr Ile Tyr Gly  
 595 600 605

aaa gtt agt aaa tcc aat att act act tct aca tca gat gca ata tca 1872  
 Lys Val Ser Lys Ser Asn Ile Thr Thr Ser Thr Ser Asp Ala Ile Ser  
 610 615 620

ata cat aac tca ata tca tgg ttt gat aaa cta act tct tgt aac acc 1920  
 Ile His Asn Ser Ile Ser Trp Phe Asp Lys Leu Thr Ser Cys Asn Thr  
 625 630 635 640

aaa act tta gca tct cgc aaa aca taa 1947  
 Lys Thr Leu Ala Ser Arg Lys Thr  
 645

<210> 22  
 <211> 648  
 <212> PRT  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 22

Met Leu Gly Asn Ser Gln Glu Ser Ser Ile Ser Ser Glu Thr Leu Glu  
 1 5 10 15

Ile Phe Ala Asp Ser Gln Ile His Ile Thr Glu Glu Gln Leu Lys Ile  
 20 25 30

Tyr Ile Lys Asn Leu Ile Asp Asn Leu Tyr Val Tyr Asn Leu Leu Asp  
 35 40 45

Pro Gly Asn Ala Ile Pro Leu Ser Ile Ile Ala Met Leu Gly Leu His  
 50 55 60

Ser Asp Phe His Ser Phe Lys Lys Ala Val Leu Asp Thr Leu Ser Gly  
65 70 75 80

Tyr Lys Asn Ser Val His Ser Phe Leu Ala Gln Ser Thr Ile Ile Asp  
85 90 95

Arg Ser Glu Ser Leu Arg Ala Glu Pro Asn His Cys Leu Tyr Ser Leu  
100 105 110

Pro Pro Leu Leu Asp Lys Arg Thr Ser Glu Asp Met Trp Asn Asp Ile  
115 120 125

Lys Glu Leu His Ile Leu Tyr His Gln Tyr Ile Ile Asn Val Ser Val  
130 135 140

Asp Lys Ser Thr Asn Ala Ile Ser Asn Thr Val Asn Ala Pro Gly Thr  
145 150 155 160

Lys Thr Cys Ser Ile Lys Ile Ser Tyr Thr Asn Pro Leu Arg Gln His  
165 170 175

Val His Tyr Phe Thr Leu Lys Thr Leu Ile Glu Tyr Tyr Asn Thr Gln  
180 185 190

Gln Thr Ser Leu Thr Gly His Arg Ser Ile Asp Asp Gln Gln Glu Ala  
195 200 205

Ala Val Thr Leu Phe Lys Glu Thr Leu Glu Glu Lys Phe Cys Lys Gly  
210 215 220

Leu Lys Asn Lys Ile Phe Phe Asn Tyr Ala Gln Tyr Leu Lys Ser Leu  
225 230 235 240

Phe Thr Ile Val Thr Ser Asn Pro Lys Val Asp Tyr Thr Leu Pro Gln  
245 250 255

Asn Ile Tyr Arg Tyr Cys Glu Thr Arg Arg Met Val Ile Ser Lys Ile  
260 265 270

Thr His Asp Ile Ile Pro Ile Ser Asp Pro Gly Thr Asp Ile Arg Ile  
275 280 285

Tyr Cys Asp Ile Pro Glu Tyr Val Thr Val Leu Ser Glu Thr Ser Asn  
290 295 300

Ile Thr Ile Tyr Gly Lys Glu Val Leu Gly Lys Val Tyr Ser Ile Tyr  
305 310 315 320

Gly Thr Ile Ile Ile Lys Asn Asn Met Pro His Asn Glu Arg Glu Ile  
325 330 335

Ser Ser Arg Ile Cys Ser Leu Phe Gly Arg Val Ile Ile Asn Gly Arg  
340 345 350

Ile Leu Asn Arg Lys His Thr Ile Pro Ser Ile Phe Glu Ile Asn Asn  
355 360 365

His Asn Thr Tyr Leu Ser Leu Lys Tyr Asn Ser Ile Leu Thr Lys Ile  
370 375 380

Thr Ser Ser Ser Val Gly Ser Val Asn Glu Glu Lys Lys Ser Gln Ile  
385 390 395 400

Phe Glu Ile Ser Arg Asp Thr Ile Leu Asn Ser Thr Asn Tyr Gln Arg  
405 410 415

Asn Ile Ser Asn Leu Lys Ile Glu Leu His Asn Pro Asp Glu Gln Leu  
420 425 430

Thr Ala Thr Val Ile Ser Leu Asp Leu Lys Asp His Pro Leu Pro Ile  
435 440 445

Thr Asn Asn Asn Thr Ile Pro Asn Ile Leu Ser Leu Thr Asp Asn His  
450 455 460

Ala Thr Asp Ser Glu Leu Pro Ser Glu Phe Phe Ser Asn Asn Val Asn  
465 470 475 480

Pro Lys Ser Ala Gly Ile Thr Arg Ile Lys Asn Thr Ile Ile Ile Glu  
485 490 495

Lys Leu Thr Pro Thr Ile Gly Arg Tyr Met Asn Val Ala Thr Lys Asn  
500 505 510



actttattta ataaagcagc agtattttaca tcagctacta taaaagcaca attaccatgc 420  
 tgcctaataa tatcacatat gttagaactg attttttctat caatatatat attatctata 480  
 atattaacta ctgaacttaa ttcataaaaa tttttatcaa gcaaaacttg ctttagaaac 540  
 ttatcataca taataaaaaa acaagctata tgctattatt gtaacttaat agctaagttt 600  
 aaaaatctct tatagtaaag tataccaata aaactaaatc ttagaaaaaa ctttctcaaa 660  
 tttaaaatat taattttttt tttacaatac gatactagaa cacacacata tattagttaa 720  
 ctacaaatac cagtgtactg ctaattcaac atataagtca ttgcttataa taacattatt 780  
 aattaaaaaa taactattct agccagtgtt catcacacta tgtcatttta cagtagatca 840  
 caacttaaag aaacaaaata ctattaaaat aacacattaa aagcatatca ataatactta 900  
 ataataacca tcaatgttta taatttatgt aaaataaaaa actttttattc ttaatcatta 960  
 cactttatgt atatattaca aatttttgaa caataataaa ttaaaactatc aagaatagtt 1020  
 gtcattttta gtttatcaca acataggaaa ttctatatcc ctattataag taacatatat 1080  
 atttaataa tacaatcaac aaataaacac actacaactg ataaggttac acctactata 1140  
 aacatataga taaataaaaa ttcaacataa ctatcaccaa tataagacaa atactgtttt 1200  
 tttgaatata ggaacattaa taacctacta taaatgtttc taactttaag tatagtacaa 1260  
 aacaaaatac tcatttttta tttatattaa atatatatat tttaactaca taaattaatt 1320  
 accattataa agaaatatat atacttgaga attatcaaaa tatttatctt actatctcaa 1380  
 ttaatatagt tgccttatct acataactgc aattgactaa cttatcacag ttgatatgat 1440  
 taagaatagc aaaattttac tttatatgtg tttatatgga gactagatgt cagcaaatcc 1500  
 cttagatcag tttaggattt ccactatatt caagctacct gatattggcg aatataatat 1560  
 tgattttact aatgcctcat tatttatggt attatccaca tttttaatct ctttgtcttg 1620  
 ctatgttgga ttaaggaaag aaagtgttat tccgaatcca ttacaatcaa taatagaaat 1680  
 tatttatgat tttattgttt ctacaataga aagtaatgta ggtaaggaag gattacaata 1740  
 cgtaccatta gtttttacia tatttacatt cattctagta tgtaatctct taggtatatt 1800  
 accattaggg ttcactgtaa caagtcatat tgcagtaaca tttgcaatat caatgattgt 1860  
 attcataagt gtaacattca taggatttaa acaccaagga actcatttcc ttcatatatt 1920  
 gttaccacaa ggcacaccaa tgtgggttagc acctatgatg gtcttaattg aattatttgc 1980

ctattgcgca cgccctgtaa gcctatcaat acgactcgct gctaatatga tagctggcca 2040  
tactattatc aagggttatag caggattcgt tataaatatg aatatatatt taacaccttt 2100  
acctatagca ttcattataa tactttattgg gtttgaaata ttcgttgcaa tcttacaggc 2160  
atacattttt acagtactca cttgtgtgta cttatcagat gcagtaaata agcactaaat 2220  
tttagcgatt gacttcgtat aatgatctac ttataattct tctagctttt tataaaggta 2280  
agagtgtatg gattctttta agtttattgc tgtagggtta agtgtttttg gtatggttgc 2340  
ttctgcttta ggggttgcaa atatatattc tactatgcta aatggattag cacgtaatcc 2400  
tgaaacagaa gataaactaa aaaaatatgt ttatactggg gctgcttttag ttgaagcaat 2460  
gggtttatatt tctttcctat tagccctatt actaattttt gtagcctaag gtagatttat 2520  
ggacacaata ccacagttag atatatcttc ttatccttct cagttttttt ggtttttttt 2580  
atcttttagt gttttgtaca ttataattag taaaaatgtg ctgccaaaga ttgaaaatat 2640  
agtaagaaag aggtataata ttataagatg ttctattgat tctgttaagg gtgatttaag 2700  
ccatgcgcag caagagttag ataaacagct gctaaagctt actgcagtac aagcagaagt 2760  
agatagaatt atacgac 2778

<210> 24  
<211> 551  
<212> DNA  
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)  
<220>  
<221> misc\_feature  
<222> (1)..(551)  
<223> Complement to SEQ ID NO:23, nucleotides <1..551  
Hypothetical AraM protein  
Product = "9hworfli"

<400> 24  
gatctacaaa taaagtcagc aaaaccacta actataagcc ttcttggcgc atttacaata 60  
atatctacat ctatatatat agctttcggg aaatgagctt ttaatgactt tttgttacca 120  
ccactaaatg ttatagatgc atttgatgaa ctatacccat tcatagaagg agctgtagga 180  
aatgaaatat aatttttatt tgtaatgtaa ctcacatatt taciaaagatc atttattgtg 240  
ccactaccaa aagatactaa aatatcagca tcttgtgatt tttctgtaat taattctact 300  
aacgtttgag atgcacaata tttttgcagg attataaaat ttttaaaagt attaaataca 360

actttattta ataaagcagc agtattttaca tcagctacta taaaagcaca attaccatgc 420  
 tgcctaataa tatcacatat gttagaactg atttttctat caatatatat attatctata 480  
 atattaacta ctgaacttaa ttcataaaaa tttttatcaa gcaaaacttg ctttagaaac 540  
 ttatcataca t 551

<210> 25  
 <211> 732  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
 <221> CDS  
 <222> (1)..(732)  
 <223> Corresponds to SEQ ID NO:23, nucleotides 1487..2218  
 Hypothetical ATP synthase A chain  
 Product = "9hworf2"

<400> 25  
 atg tca gca aat ccc tta gat cag ttt agg att tcc act ata ttc aag 48  
 Met Ser Ala Asn Pro Leu Asp Gln Phe Arg Ile Ser Thr Ile Phe Lys  
 1 5 10 15  
 cta cct gat att ggc gaa tat aat att gat ttt act aat gcc tca tta 96  
 Leu Pro Asp Ile Gly Glu Tyr Asn Ile Asp Phe Thr Asn Ala Ser Leu  
 20 25 30  
 ttt atg gta tta tcc aca ttt tta atc tcc ttg tct tgc tat gtt gga 144  
 Phe Met Val Leu Ser Thr Phe Leu Ile Ser Leu Ser Cys Tyr Val Gly  
 35 40 45  
 tta agg aaa gaa agt gtt att ccg aat cca tta caa tca ata ata gaa 192  
 Leu Arg Lys Glu Ser Val Ile Pro Asn Pro Leu Gln Ser Ile Ile Glu  
 50 55 60  
 att att tat gat ttt att gtt tct aca ata gaa agt aat gta ggt aag 240  
 Ile Ile Tyr Asp Phe Ile Val Ser Thr Ile Glu Ser Asn Val Gly Lys  
 65 70 75 80  
 gaa gga tta caa tac gta cca tta gtt ttt aca ata ttt aca ttc att 288  
 Glu Gly Leu Gln Tyr Val Pro Leu Val Phe Thr Ile Phe Thr Phe Ile  
 85 90 95  
 cta gta tgt aat ctc tta ggt ata tta cca tta ggg ttc act gta aca 336  
 Leu Val Cys Asn Leu Leu Gly Ile Leu Pro Leu Gly Phe Thr Val Thr  
 100 105 110  
 agt cat att gca gta aca ttt gca ata tca atg att gta ttc ata agt 384  
 Ser His Ile Ala Val Thr Phe Ala Ile Ser Met Ile Val Phe Ile Ser  
 115 120 125

gta aca ttc ata gga ttt aaa cac caa gga act cat ttc ctt cat ata 432  
 Val Thr Phe Ile Gly Phe Lys His Gln Gly Thr His Phe Leu His Ile  
 130 135 140

ttg tta cca caa ggc aca cca atg tgg tta gca cct atg atg gtc tta 480  
 Leu Leu Pro Gln Gly Thr Pro Met Trp Leu Ala Pro Met Met Val Leu  
 145 150 155 160

att gaa tta ttt gcc tat tgc gca cgc cct gta agc cta tca ata cga 528  
 Ile Glu Leu Phe Ala Tyr Cys Ala Arg Pro Val Ser Leu Ser Ile Arg  
 165 170 175

ctc gct gct aat atg ata gct ggc cat act att atc aag gtt ata gca 576  
 Leu Ala Ala Asn Met Ile Ala Gly His Thr Ile Ile Lys Val Ile Ala  
 180 185 190

gga ttc gtt ata aat atg aat ata ttt tta aca cct tta cct ata gca 624  
 Gly Phe Val Ile Asn Met Asn Ile Phe Leu Thr Pro Leu Pro Ile Ala  
 195 200 205

ttc att ata ata ctt att ggg ttt gaa ata ttc gtt gca atc tta cag 672  
 Phe Ile Ile Ile Leu Ile Gly Phe Glu Ile Phe Val Ala Ile Leu Gln  
 210 215 220

gca tac att ttt aca gta ctc act tgt gtg tac tta tca gat gca gta 720  
 Ala Tyr Ile Phe Thr Val Leu Thr Cys Val Tyr Leu Ser Asp Ala Val  
 225 230 235 240

aat aag cac taa 732  
 Asn Lys His

<210> 26

<211> 243

<212> PRT

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 26

Met Ser Ala Asn Pro Leu Asp Gln Phe Arg Ile Ser Thr Ile Phe Lys  
 1 5 10 15

Leu Pro Asp Ile Gly Glu Tyr Asn Ile Asp Phe Thr Asn Ala Ser Leu  
 20 25 30

Phe Met Val Leu Ser Thr Phe Leu Ile Ser Leu Ser Cys Tyr Val Gly  
 35 40 45

Leu Arg Lys Glu Ser Val Ile Pro Asn Pro Leu Gln Ser Ile Ile Glu  
 50 55 60



Ile Ile Tyr Asp Phe Ile Val Ser Thr Ile Glu Ser Asn Val Gly Lys  
65 70 75 80

Glu Gly Leu Gln Tyr Val Pro Leu Val Phe Thr Ile Phe Thr Phe Ile  
85 90 95

Leu Val Cys Asn Leu Leu Gly Ile Leu Pro Leu Gly Phe Thr Val Thr  
100 105 110

Ser His Ile Ala Val Thr Phe Ala Ile Ser Met Ile Val Phe Ile Ser  
115 120 125

Val Thr Phe Ile Gly Phe Lys His Gln Gly Thr His Phe Leu His Ile  
130 135 140

Leu Leu Pro Gln Gly Thr Pro Met Trp Leu Ala Pro Met Met Val Leu  
145 150 155 160

Ile Glu Leu Phe Ala Tyr Cys Ala Arg Pro Val Ser Leu Ser Ile Arg  
165 170 175

Leu Ala Ala Asn Met Ile Ala Gly His Thr Ile Ile Lys Val Ile Ala  
180 185 190

Gly Phe Val Ile Asn Met Asn Ile Phe Leu Thr Pro Leu Pro Ile Ala  
195 200 205

Phe Ile Ile Ile Leu Ile Gly Phe Glu Ile Phe Val Ala Ile Leu Gln  
210 215 220

Ala Tyr Ile Phe Thr Val Leu Thr Cys Val Tyr Leu Ser Asp Ala Val  
225 230 235 240

Asn Lys His

<210> 27

<211> 222

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> CDS  
 <222> (1)..(222)  
 <223> Corresponds to SEQ ID NO:23, nucleotides 2288..2509  
 Hypothetical ATP synthase C chain  
 Product = "9hworf3"

<400> 27  
 atg gat tct tta aag ttt att gct gta ggg tta agt gtt ttt ggt atg 48  
 Met Asp Ser Leu Lys Phe Ile Ala Val Gly Leu Ser Val Phe Gly Met  
 1 5 10 15

gtt gct tct gct tta ggg gtt gca aat ata ttt tct act atg cta aat 96  
 Val Ala Ser Ala Leu Gly Val Ala Asn Ile Phe Ser Thr Met Leu Asn  
 20 25 30

gga tta gca cgt aat cct gaa aca gaa gat aaa cta aaa aaa tat gtt 144  
 Gly Leu Ala Arg Asn Pro Glu Thr Glu Asp Lys Leu Lys Lys Tyr Val  
 35 40 45

tat act ggt gct gct tta gtt gaa gca atg ggt tta ttt tct ttc cta 192  
 Tyr Thr Gly Ala Ala Leu Val Glu Ala Met Gly Leu Phe Ser Phe Leu  
 50 55 60

tta gcc cta tta cta att ttt gta gcc taa 222  
 Leu Ala Leu Leu Leu Ile Phe Val Ala  
 65 70

<210> 28  
 <211> 73  
 <212> PRT  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 28  
 Met Asp Ser Leu Lys Phe Ile Ala Val Gly Leu Ser Val Phe Gly Met  
 1 5 10 15

Val Ala Ser Ala Leu Gly Val Ala Asn Ile Phe Ser Thr Met Leu Asn  
 20 25 30

Gly Leu Ala Arg Asn Pro Glu Thr Glu Asp Lys Leu Lys Lys Tyr Val  
 35 40 45

Tyr Thr Gly Ala Ala Leu Val Glu Ala Met Gly Leu Phe Ser Phe Leu  
 50 55 60

Leu Ala Leu Leu Leu Ile Phe Val Ala  
 65 70

<210> 29  
 <211> 261  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
 <221> CDS  
 <222> (1)..(261)  
 <223> Corresponds to SEQ ID NO:23, nucleotides 2519..>2778  
 Hypothetical ATP synthase B chain  
 Product="9hworf4i"

<220>  
 <221> misc\_feature  
 <222> (261)..(261)  
 <223> n = a, c, g, or t

<400> 29  
 atg gac aca ata cca cag tta gat ata tct tct tat cct tct cag ttt 48  
 Met Asp Thr Ile Pro Gln Leu Asp Ile Ser Ser Tyr Pro Ser Gln Phe  
 1 5 10 15  
 ttt tgg ttt ttt tta tct ttt agt gtt ttg tac att ata att agt aaa 96  
 Phe Trp Phe Phe Leu Ser Phe Ser Val Leu Tyr Ile Ile Ile Ser Lys  
 20 25 30  
 aat gtg ctg cca aag att gaa aat ata gta aga aag agg tat aat att 144  
 Asn Val Leu Pro Lys Ile Glu Asn Ile Val Arg Lys Arg Tyr Asn Ile  
 35 40 45  
 ata aga tgt tct att gat tct gtt aag ggt gat tta agc cat gcg cag 192  
 Ile Arg Cys Ser Ile Asp Ser Val Lys Gly Asp Leu Ser His Ala Gln  
 50 55 60  
 caa gag tta gat aaa cag ctg cta aag ctt act gca gta caa gca gaa 240  
 Gln Glu Leu Asp Lys Gln Leu Leu Lys Leu Thr Ala Val Gln Ala Glu  
 65 70 75 80  
 gta gat aga att ata cga tcn 261  
 Val Asp Arg Ile Ile Arg Xaa  
 85

<210> 30  
 <211> 87  
 <212> PRT  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
 <221> misc\_feature  
 <222> (87)..(87)  
 <223> The 'Xaa' at location 87 stands for Ser.

<220>  
 <221> misc\_feature  
 <222> (261)..(261)  
 <223> n = a, c, g, or t

<400> 30

Met Asp Thr Ile Pro Gln Leu Asp Ile Ser Ser Tyr Pro Ser Gln Phe  
 1 5 10 15

Phe Trp Phe Phe Leu Ser Phe Ser Val Leu Tyr Ile Ile Ile Ser Lys  
 20 25 30

Asn Val Leu Pro Lys Ile Glu Asn Ile Val Arg Lys Arg Tyr Asn Ile  
 35 40 45

Ile Arg Cys Ser Ile Asp Ser Val Lys Gly Asp Leu Ser His Ala Gln  
 50 55 60

Gln Glu Leu Asp Lys Gln Leu Leu Lys Leu Thr Ala Val Gln Ala Glu  
 65 70 75 80

Val Asp Arg Ile Ile Arg Xaa  
 85

<210> 31  
 <211> 3814  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 31  
 gatcgaggcc cgcggaagc tggaatgat catgaccgc gcgtcgggtca tggcggccgc 60  
 gacacgaacc tggccgacgg tgccgaccga gcgctcgggc gcgggggcgg agatggcggg 120  
 gggaggcggg ggaagagcct gcatcattcc ggcactccgg gcgcgaaggc gaacaggtcc 180  
 gacggccgca cgaacagtcc caggcccatc tggatgccga ccagcaggac gatcagcgcc 240  
 agaagcatac gcagtacgtc cggccggaac cggcccgaca gcctcgcccc gtactggggc 300  
 cccacgaccc caccgaccag caggatgggtc gacaggacga tgctgacggg ctggttgccg 360  
 cccgcctgaa gaatggtggt catggcggtg acgatgatga tctggaacag gctggtgccc 420  
 accacgaccc cggccttcat ccgcagcaca tagagcatgg ccggcaccag aatgaagccg 480  
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 <212> DNA  
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<220>  
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 Hypothetical polar organelle development protein

Product = "12hworf2i"

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ctg gac cat cgc ctg ctg gta gag cac ctc tcc gcg ggc cag atc ctc Leu Asp His Arg Leu Leu Val Glu His Leu Ser Ala Gly Gln Ile Leu 35 40 45	144
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tcg gct gcc gaa cgg cat cgg agc ggc gac ggg tac ctc tgc ggt cgg	816
Ser Ala Ala Glu Arg His Arg Ser Gly Asp Gly Tyr Leu Cys Gly Arg	
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Cys Glu Val Leu Ile His Ala Gly Ala Ala His Asp Arg Val Glu Asp	
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Leu Gly Ile Asp Arg Val Val Glu Asp Cys Val Arg Glu Arg Arg Ile	
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Gly Glu Gly Cys Val Arg Lys Gly Arg Gly Pro Pro Ile Gly Phe Arg	
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His Gly Gly Asp Arg Ser Arg Asn Phe Gly Pro Ala Phe Asp Ile Ala	
355 360 365	
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Thr Arg Leu Gly Asp Gln Gly Arg Arg Ala Leu Phe Arg His Pro His	
370 375 380	
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Gly Gly Thr Val Gly Glu Thr Ala Ala Asp Ile Val Gln Arg Leu Leu	
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Arg Pro Pro Leu Arg Leu Gly Asp Ala Phe Ala Gln Pro Val Gly Asp	
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Thr Gly Asp Leu Pro Ala Gln Phe Phe Gln Gly Gln Gly Met Pro Val	
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Val Gly Arg Asp Gln Ser Leu Phe Asp Ala Leu Gly Glu Ala Ala His	

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 Val Gly Leu Asp Leu Ala Ala Gln Leu Phe Glu Thr Gly Arg Asn Leu  
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 ggt ctc gat cga ctg gac ccg acc att cag gtt ctg ggc gat gcg cag      1488  
 Gly Leu Asp Arg Leu Asp Pro Thr Ile Gln Val Leu Gly Asp Ala Gln  
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 aac ctc gcg ccc cat cgc ctc gac cgc ctt ggc gga gcg ttc ctc cga      1536  
 Asn Leu Ala Pro His Arg Leu Asp Arg Leu Gly Gly Ala Phe Leu Arg  
 500                      505                      510  
 cgc ctt gac ctg ctc gcc gat ggc cag gac cgc gcg ctc gat ccg gtc      1584  
 Arg Leu Asp Leu Leu Ala Asp Gly Gln Asp Arg Ala Leu Asp Pro Val  
 515                      520                      525  
 cat ccg gcc ttc ggt ttc ggc tgt atc gag ccg ccg cat cat ctc ggc      1632  
 His Pro Ala Phe Gly Phe Gly Cys Ile Glu Pro Pro His His Leu Gly  
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 Ala Ile Gly Phe Asn Arg Pro Ala Gln Gly Leu Gly Glu Leu Phe Glu  
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 35                      40                      45  
 Gly Arg Arg Leu Ala Arg Asn Asn Gly Gln Gly Cys Asp Arg Leu Ser  
 50                      55                      60  
 Gly Phe Pro Arg Cys Arg Gln Ala Gly Asn Ile Gln Ala Arg Ser Arg

65                      70                      75                      80  
 Gln Leu Ser Gly Arg Ile Gly Pro Ala Gly Gly Gln Gln His Gly Asn  
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 Gly Arg Ser Ala Glu Arg Leu Ala Asn Arg Ala Thr Val Leu Ala Arg  
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 Leu Leu Phe Gln Pro Phe Leu Lys Thr Gly Leu Ala Ala Ala Leu Gln  
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 Ala Glu Ala Arg Thr Gly Arg Ser Leu Asp Gly Gly Ser Arg His Gly  
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 Arg Thr Gly Gly Val Asp Gly Leu Ala Gly Arg Gly Gly Ala Thr Leu  
                             145                      150                      155                      160  
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 Val Glu Ile Val Met Thr Ala Val Lys Gly Arg Arg Gly Pro Val Ser  
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 Gly Arg Gly Arg Leu Gln Gly Ile Arg Asp Val Arg Thr Ala Glu Ala  
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 Leu Ala Glu Ser Asp Arg Ser Ser Arg Asp Leu Asn Arg Arg Ser Ile  
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 Asp Leu Arg Arg Arg Ala Asp Phe Leu Gly Gln Arg Gly His Gly Gly  
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 Cys Glu Val Leu Ile His Ala Gly Ala Ala His Asp Arg Val Glu Asp  
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Arg Gly Val Arg Leu Gly Arg Ser Gln Ile Arg Gly Pro Gly Leu Leu  
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Leu Gly Ile Asp Arg Val Val Glu Asp Cys Val Arg Glu Arg Arg Ile  
325 330 335

Gly Glu Gly Cys Val Arg Lys Gly Arg Gly Pro Pro Ile Gly Phe Arg  
340 345 350

His Gly Gly Asp Arg Ser Arg Asn Phe Gly Pro Ala Phe Asp Ile Ala  
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Thr Arg Leu Gly Asp Gln Gly Arg Arg Ala Leu Phe Arg His Pro His  
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Pro Leu Gly Gln Phe Ala Gly Ser Ala Val Val Ala Leu Leu Asp Ala  
385 390 395 400

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Arg Pro Pro Leu Arg Leu Gly Asp Ala Phe Ala Gln Pro Val Gly Asp  
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Thr Gly Asp Leu Pro Ala Gln Phe Phe Gln Gly Gln Gly Met Pro Val  
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Asn Leu Ala Pro His Arg Leu Asp Arg Leu Gly Gly Ala Phe Leu Arg  
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Arg Leu Asp Leu Leu Ala Asp Gly Gln Asp Arg Ala Leu Asp Pro Val  
515 520 525

His Pro Ala Phe Gly Phe Gly Cys Ile Glu Pro Pro His His Leu Gly  
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Cys Cys Asp Arg Arg Ser Asp Trp Ala Met Arg Ser Leu Ser Arg Ser  
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Glu Ile Arg Val Ile Ser Pro Pro Ser Phe Ser Arg Ala Arg Ala Cys  
35 40 45  
  
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Arg Ser Ser Val Ala Ile Ser Arg Cys Ser Met Pro Trp Ala Lys Arg  
50 55 60  
  
ccc atg tcg gtc tcg acc ttg cgg ctc agc tgt tcg aaa cgg gcc gga 240  
Pro Met Ser Val Ser Thr Leu Arg Leu Ser Cys Ser Lys Arg Ala Gly  
65 70 75 80  
  
acc tcg gtc tcg atc gac tgg acc cga cca ttc agg ttc tgg gcg atg 288  
Thr Ser Val Ser Ile Asp Trp Thr Arg Pro Phe Arg Phe Trp Ala Met  
85 90 95  
  
cgc aga acc tcg cgc ccc atc gcc tcg acc gcc ttg gcg gag cgt tcc 336

Arg Arg Thr Ser Arg Pro Ile Ala Ser Thr Ala Leu Ala Glu Arg Ser  
 100 105 110

tcc gac gcc ttg acc tgc tcg ccg atg gcc agg acc gcg cgc tcg atc 384  
 Ser Asp Ala Leu Thr Cys Ser Pro Met Ala Arg Thr Ala Arg Ser Ile  
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cgg tcc atc cgg cct tcg gtt tcg gct gta tcg agc cgc cgc atc atc 432  
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 130 135 140

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 Ser Ala Arg Leu Ala Ser Thr Asp Arg Leu Arg Val Ser Ala Ser Phe  
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 35 40 45

Arg Ser Ser Val Ala Ile Ser Arg Cys Ser Met Pro Trp Ala Lys Arg  
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Pro Met Ser Val Ser Thr Leu Arg Leu Ser Cys Ser Lys Arg Ala Gly  
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 85 90 95



Arg Arg Thr Ser Arg Pro Ile Ala Ser Thr Ala Leu Ala Glu Arg Ser  
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Ser Asp Ala Leu Thr Cys Ser Pro Met Ala Arg Thr Ala Arg Ser Ile  
 115 120 125

Arg Ser Ile Arg Pro Ser Val Ser Ala Val Ser Ser Arg Arg Ile Ile  
 130 135 140

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3901

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 Product = "13hworf1"

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 Leu Glu Asp Asn Gly Ala Leu Glu Gly Tyr Asn Asp Lys Ile Met Glu  
 35 40 45  
  
 ata gta aat ggt tat caa tct ttt gat ggt aag ttt gct gag gta tta 192  
 Ile Val Asn Gly Tyr Gln Ser Phe Asp Gly Lys Phe Ala Glu Val Leu  
 50 55 60  
  
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 Pro Ile Ile Gly Leu Glu Lys Asp Phe Pro Val Val Val Val Ile Gly  
 65 70 75 80  
  
 ctg ggt aaa tct gag gat ttt gat gaa aat aaa gct tta aaa gtt ggt 288  
 Leu Gly Lys Ser Glu Asp Phe Asp Glu Asn Lys Ala Leu Lys Val Gly  
 85 90 95  
  
 ggt gta ata tat tct gaa ctt aat aga atg aag gta cca gat gca tca 336  
 Gly Val Ile Tyr Ser Glu Leu Asn Arg Met Lys Val Pro Asp Ala Ser  
 100 105 110  
  
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 Ile Val Ile Asn Thr Asp Ser Asn Val Ser Ala Asn Ile Gly Tyr Gly  
 115 120 125  
  
 gca ctt tta cgt agt ttt aaa ttt gat aaa tat ttc gta gag aaa aaa 432  
 Ala Leu Leu Arg Ser Phe Lys Phe Asp Lys Tyr Phe Val Glu Lys Lys  
 130 135 140  
  
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Asp Lys Asn Ser Val Tyr Leu Asn Lys Leu Leu Leu Phe Ser Lys Ser  
 145 150 155 160

gat cca caa gag gtt act gct ttg ttt aat gat tta aaa gct gaa ggt 528  
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 165 170 175

gag tca ata ttc tta gct cgt tct ttt gtt tca gag cct ccg aat att 576  
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 180 185 190

tta tat cca gaa acg tat gct cag atg ata tat gaa gaa tta agt aag 624  
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 Val Gly Val Thr Val Glu Val Phe Asp Glu Asp Tyr Met Lys Ala Asn  
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caa atg atg gca ctt ctt gga gta ggt cag ggt agt gct aaa aaa tct 720  
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 225 230 235 240

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 Arg Leu Val Val Met Lys Trp Asn Gly Gly Asp Glu Ser Glu Ser Pro  
 245 250 255

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 Ile Ala Phe Val Gly Lys Gly Val Thr Phe Asp Thr Gly Gly Ile Ser  
 260 265 270

tta aaa cct tca aag ggt atg tgg gat atg aaa tat gat atg gca ggt 864  
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 275 280 285

tct gct tct gtt gtt gga att atg cgt act ctt gct gca agg aag gca 912  
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 290 295 300

aaa gtt aat gct gtt gga gtg gtt gga tta gtt gaa aat tca gta gat 960  
 Lys Val Asn Ala Val Gly Val Val Gly Leu Val Glu Asn Ser Val Asp  
 305 310 315 320

gga aat gcg caa aga cct agt gat gtt gtt att tca atg tct gga caa 1008  
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aca att gag gtg tta aat act gat gca gag ggt agg ttg gtt tta gct 1056  
 Thr Ile Glu Val Leu Asn Thr Asp Ala Glu Gly Arg Leu Val Leu Ala  
 340 345 350

gat gct tta tgg tat act cag gag atg ttt act cct aaa tta atg gtg 1104  
 Asp Ala Leu Trp Tyr Thr Gln Glu Met Phe Thr Pro Lys Leu Met Val  
 355 360 365

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370 375 380  
  
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385 390 395 400  
  
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405 410 415  
  
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Phe Leu Gln Arg Phe Val Asn Gly Val Pro Trp Val His Leu Asp Ile  
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Ala Gly Met Ala Trp Asp Tyr Glu Gly Thr Glu Ile Cys Pro Lys Gly  
465 470 475 480  
  
gca act ggt ttt ggg gta agg cta tta aat aga ttt gta tca aag tac 1488  
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&lt;211&gt; 500

&lt;212&gt; PRT

&lt;213&gt; Ehrlichia ruminantium (formerly Cowdria ruminantium)

&lt;400&gt; 40

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Leu Glu Asp Asn Gly Ala Leu Glu Gly Tyr Asn Asp Lys Ile Met Glu  
35 40 45

Ile Val Asn Gly Tyr Gln Ser Phe Asp Gly Lys Phe Ala Glu Val Leu  
50 55 60

Pro Ile Ile Gly Leu Glu Lys Asp Phe Pro Val Val Val Val Ile Gly  
65 70 75 80

Leu Gly Lys Ser Glu Asp Phe Asp Glu Asn Lys Ala Leu Lys Val Gly  
85 90 95

Gly Val Ile Tyr Ser Glu Leu Asn Arg Met Lys Val Pro Asp Ala Ser  
100 105 110

Ile Val Ile Asn Thr Asp Ser Asn Val Ser Ala Asn Ile Gly Tyr Gly  
115 120 125

Ala Leu Leu Arg Ser Phe Lys Phe Asp Lys Tyr Phe Val Glu Lys Lys  
130 135 140

Asp Lys Asn Ser Val Tyr Leu Asn Lys Leu Leu Leu Phe Ser Lys Ser  
145 150 155 160

Asp Pro Gln Glu Val Thr Ala Leu Phe Asn Asp Leu Lys Ala Glu Gly  
165 170 175

Glu Ser Ile Phe Leu Ala Arg Ser Phe Val Ser Glu Pro Pro Asn Ile  
180 185 190

Leu Tyr Pro Glu Thr Tyr Ala Gln Met Ile Tyr Glu Glu Leu Ser Lys  
195 200 205

Val Gly Val Thr Val Glu Val Phe Asp Glu Asp Tyr Met Lys Ala Asn  
210 215 220

Gln Met Met Ala Leu Leu Gly Val Gly Gln Gly Ser Ala Lys Lys Ser  
225 230 235 240

Arg Leu Val Val Met Lys Trp Asn Gly Gly Asp Glu Ser Glu Ser Pro  
245 250 255

Ile Ala Phe Val Gly Lys Gly Val Thr Phe Asp Thr Gly Gly Ile Ser  
260 265 270

Leu Lys Pro Ser Lys Gly Met Trp Asp Met Lys Tyr Asp Met Ala Gly  
275 280 285

Ser Ala Ser Val Val Gly Ile Met Arg Thr Leu Ala Ala Arg Lys Ala  
290 295 300

Lys Val Asn Ala Val Gly Val Val Gly Leu Val Glu Asn Ser Val Asp  
305 310 315 320

Gly Asn Ala Gln Arg Pro Ser Asp Val Val Ile Ser Met Ser Gly Gln  
325 330 335

Thr Ile Glu Val Leu Asn Thr Asp Ala Glu Gly Arg Leu Val Leu Ala  
340 345 350

Asp Ala Leu Trp Tyr Thr Gln Glu Met Phe Thr Pro Lys Leu Met Val  
355 360 365

Asp Leu Ala Thr Leu Thr Gly Ala Val Val Val Ala Leu Gly Asn Asn  
370 375 380

Gln Tyr Ala Gly Leu Phe Ser Asn Asp Asp Ser Ile Ala Asn Gln Leu  
385 390 395 400

Ile Val Ala Gly Asn Glu Ser Gly Glu Lys Leu Trp Arg Leu Pro Leu  
405 410 415

Asp Glu Ala Tyr Asp Lys Leu Ile Asp Ser Ser Ile Ala Asp Met Gln  
420 425 430

Asn Ile Ser Thr Lys Gly Tyr Gly Ala Asp Ser Ile Thr Ala Ala Gln  
435 440 445

Phe Leu Gln Arg Phe Val Asn Gly Val Pro Trp Val His Leu Asp Ile  
450 455 460

Ala Gly Met Ala Trp Asp Tyr Glu Gly Thr Glu Ile Cys Pro Lys Gly  
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485

490

495

Tyr Glu Ser His  
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Product = "13hworf2"

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20 25 30  
  
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Ala Ser Val Ser Cys Val Ile Ser Asn Lys Ser Asn Ala Asn Gly Leu  
35 40 45  
  
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Ile Leu Ala Gln Gln Ser Asn Ile Lys Thr Phe Ile Val Gln Gly Arg  
50 55 60  
  
cct cta gat ttt gat gct att gat aat ata ctt gaa gaa cat gag gtg 240  
Pro Leu Asp Phe Asp Ala Ile Asp Asn Ile Leu Glu Glu His Glu Val  
65 70 75 80  
  
gat tta atc tgt ctt gca gga ttt atg agt att gtt cct gaa aag ttt 288  
Asp Leu Ile Cys Leu Ala Gly Phe Met Ser Ile Val Pro Glu Lys Phe  
85 90 95  
  
att aat aag tgg tta tat aag gtt att aat ata cat cct tct ctc ttg 336  
Ile Asn Lys Trp Leu Tyr Lys Val Ile Asn Ile His Pro Ser Leu Leu  
100 105 110  
  
cca tca ttt aag ggt tta aat gca caa gct caa gca tta aag gct gga 384  
Pro Ser Phe Lys Gly Leu Asn Ala Gln Ala Gln Ala Leu Lys Ala Gly  
115 120 125  
  
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Ala Ser Val Ser Cys Val Ile Ser Asn Lys Ser Asn Ala Asn Gly Leu
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Ile Leu Ala Gln Gln Ser Asn Ile Lys Thr Phe Ile Val Gln Gly Arg
          50          55          60

Pro Leu Asp Phe Asp Ala Ile Asp Asn Ile Leu Glu Glu His Glu Val
65          70          75          80

Asp Leu Ile Cys Leu Ala Gly Phe Met Ser Ile Val Pro Glu Lys Phe
          85          90          95

Ile Asn Lys Trp Leu Tyr Lys Val Ile Asn Ile His Pro Ser Leu Leu

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105

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 130 135 140

Gly Gly Pro Ile Ile Val Gln Ala Ala Val Pro Val Phe Ser Ser Asp  
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Ser Val Glu Asp Leu Ala Asn Arg Ile Leu Lys Met Glu His Ile Cys  
 165 170 175

Tyr Pro Lys Ala Val Glu Leu Ile Ala Tyr Asn Gln Leu Gln Leu Asn  
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 195 200 205

Glu Ala Phe Val  
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 Product = "13hworf3i"

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 <223> Xaa = Ser

<400> 43  
 atg gag tgg aag att gaa tcc tta cct gta cct tat gat aaa gct atg 48  
 Met Glu Trp Lys Ile Glu Ser Leu Pro Val Pro Tyr Asp Lys Ala Met  
 1 5 10 15  
  
 tgt ttt atg caa caa agg gtc gag ggt att gct aat aag aca caa gat 96  
 Cys Phe Met Gln Gln Arg Val Glu Gly Ile Ala Asn Lys Thr Gln Asp  
 20 25 30  
  
 gaa cta gta tgg tta ctt gaa cat ttt ccg tta tat acg gct ggt act 144  
 Glu Leu Val Trp Leu Leu Glu His Phe Pro Leu Tyr Thr Ala Gly Thr  
 35 40 45  
  
 agt gca agg agt gag gaa tta cta acc gat agt tta ttt cct gta tat 192  
 Ser Ala Arg Ser Glu Glu Leu Leu Thr Asp Ser Leu Phe Pro Val Tyr  
 50 55 60  
  
 tct aca ggt aga ggt ggt aaa tac act tat cat ggt cct ggt caa aga 240  
 Ser Thr Gly Arg Gly Gly Lys Tyr Thr Tyr His Gly Pro Gly Gln Arg  
 65 70 75 80  
  
 att gct tat gtg atg atg gat tta aaa gca aga gat aaa tgt aat gtt 288  
 Ile Ala Tyr Val Met Met Asp Leu Lys Ala Arg Asp Lys Cys Asn Val  
 85 90 95  
  
 agg ttg tat gtt gaa act ttg ggt gag tgg att gtt aaa act tta aag 336  
 Arg Leu Tyr Val Glu Thr Leu Gly Glu Trp Ile Val Lys Thr Leu Lys  
 100 105 110  
  
 cat ttt tca ata cga tcn 354  
 His Phe Ser Ile Arg  
 115

<210> 44  
 <211> 117  
 <212> PRT  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
 <221> misc\_feature  
 <222> (354)..(354)  
 <223> n = a, c, g, or t

<220>  
 <221> misc\_feature  
 <222> (352)..(354)  
 <223> Xaa = Ser

<400> 44  
 Met Glu Trp Lys Ile Glu Ser Leu Pro Val Pro Tyr Asp Lys Ala Met  
 1 5 10 15

Cys Phe Met Gln Gln Arg Val Glu Gly Ile Ala Asn Lys Thr Gln Asp  
20 25 30

Glu Leu Val Trp Leu Leu Glu His Phe Pro Leu Tyr Thr Ala Gly Thr  
35 40 45

Ser Ala Arg Ser Glu Glu Leu Leu Thr Asp Ser Leu Phe Pro Val Tyr  
50 55 60

Ser Thr Gly Arg Gly Gly Lys Tyr Thr Tyr His Gly Pro Gly Gln Arg  
65 70 75 80

Ile Ala Tyr Val Met Met Asp Leu Lys Ala Arg Asp Lys Cys Asn Val  
85 90 95

Arg Leu Tyr Val Glu Thr Leu Gly Glu Trp Ile Val Lys Thr Leu Lys  
100 105 110

His Phe Ser Ile Arg  
115

<210> 45

<211> 4369

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 45

gatcctctga ttgaggaaga tcaacaccac aatgtttttc tttagtgtga tacataacat 60

gatcaggata gaaactaggc actaacttac tagttgcctc ttcgtatata ggattaccat 120

ttctgtcaaa atctaacatt aaagaacaag tttcacttaa accacgagta tttcttaaac 180

tatcttcaac agtattaacc aaattcaaac ttgaaactaa ttggaacgta ctttcttttc 240

caacacatat aacaggotta ctatccttaa cagtagtttc acaactagaa gcagataaaa 300

ctgaatcctc tattttacct aaatctacac ctgatagttt tactttatca tcttttacat 360

taccactttg aaaattaaaa gtagcaccaa cacttctagc aacactactg tccttttcat 420

ctcttatagc agtaccttca gatactactt ttttctctac agatttatcc ttagtactac 480

ctgtacactc tgtatcagta acatcccttt tctcatctgg tttctctaata ctagaaccag 540

ataatctaac ttgattactt ttcatatcac cagtttgagc actcgactt acaaaaacat 600

ctctctttttt ttcatttatt cttatagtat caccttcagg tactactttt ttctctacag	660
atttatcctt agtatcaacc ataacatcag atttaaaact aagacttggt tttatagtag	720
tttcagtatg actatagtga acaccaacac cagcattttt cttaaccata acttggtgac	780
cttctacact atcgcgttct acagtttgaa cgtcagaaat ttgatgtgtt acctgatcca	840
ttttggtaga tgagacagta gattttgatt ttaaaacatg acctatatca tcactatcat	900
tatggtaaac tgattttaga aattcaatac catcttttcc agataaagtg tccatttcgt	960
acttttcata ttcactctga ctacaataag taaccctact ttttgatatca ttatctgata	1020
tatctaattc tcttgactta tacttcataa cactcaacac ataacatata aacctaacca	1080
caagcagaac atagtaaaca catataaaaa acagcgacac tgctgtgtat aggattatct	1140
cattcatatt atttaataag aaaattaata taagttaata tatacatata tatttaacaa	1200
ctaaaagaat tataataaaa aaatttacta tttctaatat ttttttaatt agttactaaa	1260
tctatattat attttttaaat aatactaatt tttaataata ataaactaat atcaaatgat	1320
aatcttttac tatattagca acatcataaa gtgctaaata ctacttctta tagaggatga	1380
tctactatca ctcatcacac aactcacatt aatataagat ggtaaccttt ctgaaggagt	1440
atatatttta ttcttcttaa cccgttttac aacattactt ataataatag catctgaaat	1500
ttctcccata ttgtttttta aatattcttt aactacaaca gcagcttttt tctccatctt	1560
atcactaaaa aatgaagcca atttctgaat agatttcaat atatcaagtt cccatttatc	1620
attatttatc accttagaca ttaatgtacc aaacactgaa ctttgagaat gatttccatg	1680
ttctagatat ctggttacca tattatgtac agccctatat ttaagtcgca ttttactaac	1740
cgccatgatc aaaacattct tatatgctac tgtgatcgct tctttttgaa tactctcata	1800
tacttggtgtg acatattcag aatacatata agattttact tgattctcta attcacagat	1860
caaaaaactct cgatcacagg gattagcatc acatactctc atatcctttg ccaataagta	1920
aacacattct tttataagtc ctgctttaga ctttttatac aatgttgtag cacgctgaat	1980
agcaaagtcc cgtatcataa caggcattac ttgtttatcc atacgttgta tagtattcaa	2040
catcagacta tatgcatcca tacattcatg cttaacttta ctacgtaaata tctcatcacc	2100
tattcccgac aacagagtat ctagtctatc actctcaata ttccatgctg atatcaataa	2160
atcatgagga tcaatttgca ttctccttg tgctttgtgg taaaccatta tttgagatat	2220
gtcacattca tcatctctaa acaagtatgt agtagtactt aaaccttgct tcttctttaa	2280

cttatctgta ttcaaacaag tagactcttg acctataact ctaccttcac tttcaatact 2340  
 atgtttttaca gatggtaata cagtacaatc tacactactt tcattttttc tacttttcacg 2400  
 aacacgatta gtatcatgaa taccacctat tttactagaa gccacactaa ttttctggcc 2460  
 atgactaatt gctggagtta ctaatgacaa tctagcacga cttataggcg tagcctcttt 2520  
 tctcctacta cgctcatcag catctttaac atgcctagca tcactcttct taccagtaac 2580  
 tgacctaaact gcttgatcac aaacaaccaa tctcttacta ttagcatgta cttttttatc 2640  
 tcttgcatth atcattgcta cagatctggt accactctca actatagcac gccccgcata 2700  
 cattatagct tctcgaaaaa cttgcggatt actaaaaatc aaggacatac tagtcattgg 2760  
 atcattaaac atcaaataca tattaattcg tggattacta aacattaagc ttacattcag 2820  
 acacacattt gacaatagtt tgaatagatt ttcacagttc atacttgtca tctgacttaa 2880  
 caattgttga tcaccagcat taccacttat catactcctg attacaagtc ttaaattctcg 2940  
 tgaagatata gcagtctggt tattatcaga aacagcagta cttgtactac taaccttttt 3000  
 agaatatgaa aattgtgcac aagaatctga tgggtttacca gttgtatcat cttgaccaac 3060  
 taggaaacta tgttcagatg atataatccc ttccaaacct ttatatgatg tatctgaaat 3120  
 agtatctcgc atattaatac cacgaatagc aaggctcactc atatcacaac cagtagactt 3180  
 agtatcttca tgcttagata aattttctcaa caagccagta tcagcacttg caaacacaaa 3240  
 atcgttctgt ttatcaggcc gaacaataaa gtcattccca cctaaactat ggttaagttt 3300  
 tccaagactg ccatgaaatc caacttctat cctatattgt tgagagaaaag tagatctatc 3360  
 caataatcca ccaacaccaa taaaactatc actagcatac tgcccaactc ttggattatc 3420  
 acccatacaa aaactatccg gaaaaaact acgcttttga gacaaataac tattgaaatg 3480  
 ttcaacttct gataataagt tagttgtgga ataagagcgc tttttttgaa caccaccttc 3540  
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 aggtttaccc cattcttcta tatcgccact aaaaaattta tcccattttt ctataccacc 3660  
 actaaaagggt ttactccatc tttcgagact attaccagta agaacaccat cttcttgtaa 3720  
 tcttttatca ctttgtccgt tatatagaaa ttgatcacca catttagatt ctacatcctc 3780  
 catctccatg tacgtcatat catctacacc ctacaggggaa ctttcactat cttgatcact 3840  
 tgaattaaca ttttcatcat cagaagaacc cactacacca gcacaatctt ttcgttcttg 3900

tgattcctca ctaggtatag ttttagaact tactgaagaa gcctcagatt ccccatccag 3960  
 attactatatt gttaaagtat ttcttccttc tcttccatag attttcttac aacaatacac 4020  
 tatacaacta gcaattacga gcataataat gaacaccgta aatacaataa gcattagcat 4080  
 tcttatattc atatttaata cttctttata gattatcatt aataatatat aattttttta 4140  
 tataaacaag actatttaat aaaaatatac tattttaacg gagattttta tgataattct 4200  
 taaaattata aatatatc ataacatgta acaagttatt gatataaaaa ataaaataat 4260  
 attaacctta ctaagttata ttctaaaata attaaaaata atcttaaaat ctattaataa 4320  
 gtacttatat acaattatat aataccatta ctaaataacc atacagatc 4369

<210> 46  
 <211> 1147  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
 <221> misc\_feature  
 <222> (1)..(1147)  
 <223> Complement to SEQ ID NO:45, nucleotides <1..1147  
 Product = "14hworfli"

<400> 46  
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 ttctgtcaaa atctaacatt aaagaacaag tttcacttaa accacgagta tttcttaaac 180  
 tatcttcaac agtattaacc aaattcaaac ttgaaactaa ttggaacgta ctttcttttc 240  
 caacacatat aacaggctta ctatccttaa cagtagtttc acaactagaa gcagataaaa 300  
 ctgaatcctc tattttacct aaatctacac ctgatagttt tactttatca tcttttacat 360  
 taccactttg aaaattaaaa gtagcaccaa cacttctagc aacactactg tccttttcat 420  
 ctcttatagc agtaccttca gatactactt ttttctctac agatttatcc ttagtactac 480  
 ctgtacactc tgtatcagta acatcccttt tctcatctgg tttctctaata ctagaaccag 540  
 ataatactaac ttgattactt ttcatatcac cagtttgagc actcgactt acaaaaacat 600  
 ctctcttttt ttcatttatt cttatagtat caccttcagg tactactttt ttctctacag 660  
 atttatcctt agtatcaacc ataacatcag atttaaaact aagacttggt tttatagtag 720  
 tttcagtatg actatagtga acaccaacac cagcattttt ctttaaccata acttggtgac 780



cttctacact atcgcgttct acagtttgaa cgtcagaaat ttgatgtgtt acctgatcca 840  
 ttttggtaga tgagacagta gattttgatt ttaaaacatg acctatatca tcaactatcat 900  
 tatggtaaac tgattttaga aattcaatac catcttttcc agataaagtg tccatttcgt 960  
 acttttcata ttcactctga ctacaataag taaccctact ttttgtatca ttatctgata 1020  
 tatctaattc tcttgactta tacttcataa cactcaacac ataacatata aacctaacca 1080  
 caagcagaac atagtaaaca catataaaaa acagcgacac tgctgtgtat aggattatct 1140  
 cattcat 1147

<210> 47  
 <211> 2766  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)  
 <220>  
 <221> misc\_feature  
 <222> (1)..(2766)  
 <223> Complement to SEQ ID NO:45, nucleotides 1354..4119  
 Hypothetical lipoprotein  
 Product = "14hworf2"

<400> 47  
 ctaaatacta cttcttatag aggatgatct actatcactc attacacaac tcacattaat 60  
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 attacttata ataatagcat ctgaaatttc tcccatattg ttttttaaatt attctttaac 180  
 tacaacagca gcttttttct ccatcttatc actaaaaaat gaagccaatt tctgaataga 240  
 tttcaatata tcaagttccc atttatcatt atttatcacc ttagacatta atgtaccaa 300  
 cactgaactt tgagaatgat ttccatgttc tagatatctg gttaccatat tatgtacagc 360  
 cctatattta agtcgcattt tactaaccgc catgatcaaa acattcttat atgctactgt 420  
 gatcgcttct ttttgaatac tctcatatac ttgtgtgaca tattcagaat acatataaga 480  
 ttttacttga ttctctaatt cacagatcaa aaactctcga tcaccgggat tagcatcaca 540  
 tactctcata tcttttgcca ataagtaaac acattctttt ataagtcctg cttagacct 600  
 tttatacaat gttgtaccac gctgaatagc aaagtcccgat atcataacag gcattacttg 660  
 tttatccata cgttgtatag tattcaacat cagactatat gcatccatac attcatgctt 720  
 aactttacta cgtaaattct catcacctat tcccgacaac agagtatcta gtctatcact 780

ctcaatattc catgctgata tcaataaatc atgaggatca atttgcatte ctccttgtgc 840  
 tttgtggtaa accattatatt gagatatgtc acattcatca tctctaaaca agtatgtagt 900  
 agtacttaaa ccttgcttct tctttaactt atctgtattc aaacaagtag actcttgacc 960  
 tataactcta ccttcacttt caatactatg ttttacagat ggtaatacag tacaatctac 1020  
 actactttca ttttttctac tttcacgaac acgattagta tcatgaatac cacctatttt 1080  
 actagaagcc acactaattt tctggccatg actaattgct ggagtacta atgacaatct 1140  
 agcacgactt ataggcgtag cctcttttct cctactacgc tcatcagcat ctttaacatg 1200  
 cctagcatca ctcttcttac cagtaactga cctaactgct tgatcacaaa caaccaatct 1260  
 cttactatta gcatgtactt ttttatctct tgcatttate attgctacag atctgttacc 1320  
 actctcaact atagcacgcc cgcatacat tatagcttct cgaaaaactt gcggattact 1380  
 aaaaatcaag gacatactag tcattggatc attaaacatc aaatacatat taattcgtgg 1440  
 attactaaac attaaactta cattcagaca cacatttgac aatagtttga atagattttc 1500  
 acagttcata cttgtcatct gacttaacaa ttgttgatca ccagcattac cacttatcat 1560  
 actcctgatt acaagtctta aatctcgtga agatatagca gtctgggttat tatcagaaac 1620  
 agcagtactt gtactactaa cctttttaga atatgaaaat tgtgcacaag aatctgatgg 1680  
 tttaccagtt gtatcatctt gaccaactag gaaactatgt tcagatgata taatcccttc 1740  
 caaaccttta tatgatgtat ctgaaatagt atctcgata ttaataccac gaatagcaag 1800  
 gtcactcata tcacaaccag tagacttagt atcttcatgc ttagataaat ttctcaacaa 1860  
 gccagtatca gcacttgcaa acacaaaatc gttctgttta tcaggccgaa caataaagtc 1920  
 attcccacct aaactatggg taagttttcc aagactgcc tgaaatccaa cttctatcct 1980  
 atattgttga gagaaagtag atctatccaa taatccacca acaccaataa aactatcact 2040  
 agcactatgc ccaactcttg gattatcacc catacaaaaa ctatccggaa aaacactacg 2100  
 ctttgagac aaataactat tgaaatgttc aacttctgat aataagttag ttgtggaata 2160  
 agagcgcttt ttttgaacac caccttcaact atcatactga tttaatattc tataaggtct 2220  
 atcccatctc tgtataccat cactaaaagg tttaccccat tcttctatat cgccactaaa 2280  
 aaatttatcc catttttcta taccaccact aaaagggtta ctccatcttt cgagactatt 2340  
 accagtaaga acaccatctt cttgtaatct tttatcaact tgtccgttat atagaaattg 2400

atcaccacat ttagattcta catcctccat ctccatgtac gtcatatcat ctacaccctc 2460  
 aggggaactt tcactatctt gatcacttga attaacatctt tcatcatcag aagaaccac 2520  
 tacaccagca caatcttttc gttcttgtga ttcctcacta ggtatagttt tagaacttac 2580  
 tgaagaagcc tcagattccc catccagatt actatttgggt aaagtatttc ttccttctct 2640  
 tccatagatt ttcttacaac aatacactat acaactagca attacgagca taataatgaa 2700  
 caccgtaaat acaataagca ttagcattct tatattcata tttaatactt ctttatagat 2760  
 tatcat 2766

<210> 48

<211> 3500

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 48

gatcaaaaga aattggaata tcttcaacat aaaataggga ctcatgtgct aaattaacta 60  
 aattttttgt tctctttttt agttcattaa ttccatttag tagatagcct attttctctg 120  
 tattgacttt atatcctatt gttttctcta tgaatattat atcaaattta atcttgtaaa 180  
 gtataaaacc ttgggtcttt atttactgta atgaaagtat aattattctt aatttactct 240  
 aaaatataca ataagaagtt atatctattt ttttatattt attacttaat gactcatata 300  
 tctatgattg cattgtaatt atattagtaa atctagtgtc atggatgatc tgtatctcac 360  
 tactgattta gttactgttg ttttttgat aaatgataat aaacttatta caaattgttt 420  
 tatggcaaaa tttcaataat atttggtttt catatattga cttcagtata aatttatagt 480  
 agcttttagca ctctatcttt taccagggtt atgatgataa gaatctttct tttgttaggc 540  
 ttagtattat tagtagcaag ttttccacta ttaaataact ggctatctaa tcattctgggt 600  
 aagtctacta cattggataa ggatgcagtt atatctatag ttgaggaata tataaccaat 660  
 tatcctcaga gggtaataga tttacttact acaggccaag cacaagcaga aagagcagag 720  
 cttactgaaa atattaaaaa atataaatct gagcttgaag atattgcata cccatctgct 780  
 ggcaataaag acagtaaaat tgcatttatt gagttcttcg attactcttg tggttattgt 840  
 aaaatgatgt ttgaagatat caaacaatt ataaaagatg gtaaggtagc tgttattttt 900  
 agagattttc caatacttgg ggaatcgctg ttaaaggctg ttaaagcagc attggctgta 960  
 catcttatca atccaagtaa atacttggac ttctattatg cagcattaaa tcataaacag 1020

ccatttaatg atgaatctat acttaatatata gttaaatacac ttgaaatttc agaagaggaa 1080  
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 aatctggctg agaagttaaa tatcagaggt actcctgctc ttataatagg tgatgcattc 1200  
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 gatagtcaa taatggcact tgctatagca ataattataa ttattatatt tttattatta 1500  
 acctcaaagt ggtataacaa tgatattgtt ataatactaa aaagtataat taatcctgct 1560  
 gtaaatacac aacataggggt ttttttggga tatgggtgct gttgagttgg tttttttgta 1620  
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 gtactagtgt gagggtagtg aattgctaaa gcttgtgctg tagcgtatat attaggaata 1740  
 tataattgag ccatagaaaa tcccttagct aacaatgata caggttgat atattgatca 1800  
 attgaaaatt ttaattgatc actcaatata ttatcaccaa cctttttaac tacatcatgt 1860  
 gataggcaaa tatttccatt tttatcaact aaaggacaaa ctaacttttg tatatcgaaa 1920  
 ggagagagca attgtgatgt tgtaattgat gacacagtat cccaagaaac aactcctga 1980  
 agtccttctt caaatgcttt aagtagtgga tattgtaggt tcttagcact attacacaat 2040  
 agatctatat ttcgtactat aggaattgaa actagaatat taaataataa aaattgtatg 2100  
 gaagatgttt gggctgtaca taaatattga gaaaattgct catcactgaa agaacttaca 2160  
 taacatgcag ctaattgtat ggtacgacta aacaaagaaa tgtcaaagtt ttggcatgat 2220  
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 gtattgcaga actcagtact gtacagtgt tcttgtgttg ttactatatg atctgtatcg 2340  
 acacctaatt cctctgaaaa agaatacagg acattatgta ttgtcatata gttgtgaaaa 2400  
 ggttcagcat tggtttttgc aaaatcatca gctgatgcat aatggatatag gttatttaca 2460  
 tcgctgttta gtagatttgc tagtaaagaa agtggttatat aaaacttatt aatacctgat 2520  
 gttacatgtg ataataagggt ttcagggttg ttataagcaa catatgcaat atcaaataat 2580  
 cttgtaatgc aagatttttc taaaaaatta ccaaacata gctttaataa aattattagt 2640  
 acactgctag aatagtgttc cggatcaaga gaatgttgcc ctaatactct acacattata 2700

actgagattt gtcgagcttt tctttcatta acagtactac aacaagctat catgtgatat 2760  
ggtaattgtg tattgcctaa tatgtatggg acaccttcat taaatgtag gtgttgcaat 2820  
aacatgacca tggtatttgg tataatctga gtatttttat tatatatatt agctgtgcta 2880  
caatgtaact ttgcttgaat ttcattaaaa agtacttcat acccccgaag taatttgatc 2940  
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tcttgtattt ttgaagctgg taattttaga tggaatgcgg aataataaca aagggctagt 3060  
aactctaaca aatgtcctga taattgtttg tgagctccat gtaattctgc taatatgtct 3120  
ctatagtctt tactttgcga aataaacttt tgtaatagta cttccttata tattgcactt 3180  
atgacatgta atgtatttaa ctttatggca taagtagtat taagtgtact gcgtattgca 3240  
catgagatat cgcaactaat aaaactagtg ttattgcgtg ggataacttg aaatgtactt 3300  
gttgtttgta agttttcaaa gggtctcatt gtacagttaa tgtcttgaga aagagatgct 3360  
gacattaagt actttggact gcagatagag agacaatcct ggtacattgc atagaaaata 3420  
tccttatagg cattaagtat taatctagtt aacttgccaa cttttttggt ttcgtatact 3480  
gtattagata aagatagatc 3500

<210> 49  
<211> 753  
<212> DNA  
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)  
<220>  
<221> CDS  
<222> (1)..(753)  
<223> Corresponds to SEQ ID NO:48, nucleotides 511..1263  
Hypothetical outer membrane protein  
Product = "18hworf1"

<400> 49  
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act aca ttg gat aag gat gca gtt ata tct ata gtt gag gaa tat ata 144  
Thr Thr Leu Asp Lys Asp Ala Val Ile Ser Ile Val Glu Glu Tyr Ile  
35 40 45

acc aat tat cct cag agg gta ata gat tta ctt act aca ggc caa gca 192  
 Thr Asn Tyr Pro Gln Arg Val Ile Asp Leu Leu Thr Thr Gly Gln Ala  
 50 55 60

caa gca gaa aga gca gag ctt act gaa aat att aaa aaa tat aaa tct 240  
 Gln Ala Glu Arg Ala Glu Leu Thr Glu Asn Ile Lys Lys Tyr Lys Ser  
 65 70 75 80

gag ctt gaa gat att gca tac cca tct gct ggc aat aaa gac agt aaa 288  
 Glu Leu Glu Asp Ile Ala Tyr Pro Ser Ala Gly Asn Lys Asp Ser Lys  
 85 90 95

att gca ttt att gag ttc ttc gat tac tct tgt ggt tat tgt aaa atg 336  
 Ile Ala Phe Ile Glu Phe Phe Asp Tyr Ser Cys Gly Tyr Cys Lys Met  
 100 105 110

atg ttt gaa gat atc aaa caa att ata aaa gat ggt aag gta cgt gtt 384  
 Met Phe Glu Asp Ile Lys Gln Ile Ile Lys Asp Gly Lys Val Arg Val  
 115 120 125

att ttt aga gat ttt cca ata ctt ggg gaa tcg tcg tta aag gct gtt 432  
 Ile Phe Arg Asp Phe Pro Ile Leu Gly Glu Ser Ser Leu Lys Ala Val  
 130 135 140

aaa gca gca ttg gct gta cat ctt atc aat cca agt aaa tac ttg gac 480  
 Lys Ala Ala Leu Ala Val His Leu Ile Asn Pro Ser Lys Tyr Leu Asp  
 145 150 155 160

ttc tat tat gca gca tta aat cat aaa cag cca ttt aat gat gaa tct 528  
 Phe Tyr Tyr Ala Ala Leu Asn His Lys Gln Pro Phe Asn Asp Glu Ser  
 165 170 175

ata ctt aat ata gtt aaa tca ctt gaa att tca gaa gag gaa ttt aaa 576  
 Ile Leu Asn Ile Val Lys Ser Leu Glu Ile Ser Glu Glu Glu Phe Lys  
 180 185 190

gat tct tta tct aaa aat tct agt act att gat aag atg ata gag tcc 624  
 Asp Ser Leu Ser Lys Asn Ser Ser Thr Ile Asp Lys Met Ile Glu Ser  
 195 200 205

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 Thr Arg Asn Leu Ala Glu Lys Leu Asn Ile Arg Gly Thr Pro Ala Leu  
 210 215 220

ata ata ggt gat gca ttc att ggg gga gct gca gat tta tca act tta 720  
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aga agt aaa ata gta gaa cag cag gaa caa taa 753  
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&lt;210&gt; 50

<211> 250  
 <212> PRT  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 50

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Thr Thr Leu Asp Lys Asp Ala Val Ile Ser Ile Val Glu Glu Tyr Ile  
 35 40 45

Thr Asn Tyr Pro Gln Arg Val Ile Asp Leu Leu Thr Thr Gly Gln Ala  
 50 55 60

Gln Ala Glu Arg Ala Glu Leu Thr Glu Asn Ile Lys Lys Tyr Lys Ser  
 65 70 75 80

Glu Leu Glu Asp Ile Ala Tyr Pro Ser Ala Gly Asn Lys Asp Ser Lys  
 85 90 95

Ile Ala Phe Ile Glu Phe Phe Asp Tyr Ser Cys Gly Tyr Cys Lys Met  
 100 105 110

Met Phe Glu Asp Ile Lys Gln Ile Ile Lys Asp Gly Lys Val Arg Val  
 115 120 125

Ile Phe Arg Asp Phe Pro Ile Leu Gly Glu Ser Ser Leu Lys Ala Val  
 130 135 140

Lys Ala Ala Leu Ala Val His Leu Ile Asn Pro Ser Lys Tyr Leu Asp  
 145 150 155 160

Phe Tyr Tyr Ala Ala Leu Asn His Lys Gln Pro Phe Asn Asp Glu Ser  
 165 170 175

Ile Leu Asn Ile Val Lys Ser Leu Glu Ile Ser Glu Glu Glu Phe Lys  
 180 185 190

Asp Ser Leu Ser Lys Asn Ser Ser Thr Ile Asp Lys Met Ile Glu Ser

195

200

205

Thr Arg Asn Leu Ala Glu Lys Leu Asn Ile Arg Gly Thr Pro Ala Leu  
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Arg Ser Lys Ile Val Glu Gln Gln Glu Gln  
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<210> 51  
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 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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 <223> Complement to SEQ ID NO:48, nucleotides 1275..>3500  
 Product = "18hworf2i"

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<210> 52

<211> 4750

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

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<211> 371  
<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> misc\_feature

<222> (1)..(371)

<223> Complement to SEQ ID NO:52, nucleotides <1..371  
Hypothetical integrase/recombinase  
Product = "19hworfli"

<400> 53

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ttatgcaaga actctataaa cttatcaagg tctcttacat aagaaacaac tgtattcaaa      300
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<210> 54

<211> 984

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> CDS

<222> (1)..(984)

<223> Corresponds to SEQ ID NO:52, nucleotides 632..1615  
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Product = "19hworf2"

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att gca ctg tca gca cat ggt ata tca gtt aac tta tgg gga cgt gat      96
Ile Ala Leu Ser Ala His Gly Ile Ser Val Asn Leu Trp Gly Arg Asp
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cat aga aat att aca cat ata aac act tac cga aaa aat tta aaa tat      144
His Arg Asn Ile Thr His Ile Asn Thr Tyr Arg Lys Asn Leu Lys Tyr
35           40           45

tta ccc aca tat cat cta cca gac aac ata tat gca acc agc aat ata      192
Leu Pro Thr Tyr His Leu Pro Asp Asn Ile Tyr Ala Thr Ser Asn Ile
50           55           60

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 85 90 95

atg tgt aaa aat act cca ata tta att tgt agt aaa ggt atc gaa att 336  
 Met Cys Lys Asn Thr Pro Ile Leu Ile Cys Ser Lys Gly Ile Glu Ile  
 100 105 110

aca tca ctc aaa ttt ccc agt gaa ata gca gaa gaa att tta caa tat 384  
 Thr Ser Leu Lys Phe Pro Ser Glu Ile Ala Glu Glu Ile Leu Gln Tyr  
 115 120 125

aat cca att ttt ata ctc tct ggt cca agt ttt gct aaa gaa att gca 432  
 Asn Pro Ile Phe Ile Leu Ser Gly Pro Ser Phe Ala Lys Glu Ile Ala  
 130 135 140

gaa cat ctt cct tgt agt ata gta ctt gct ggt gat aat aaa gaa ctt 480  
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 165 170 175

tac cat caa gat att ata ggt gta cag att gga gct gca tta aag aac 576  
 Tyr His Gln Asp Ile Ile Gly Val Gln Ile Gly Ala Ala Leu Lys Asn  
 180 185 190

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 195 200 205

aat gct gtt gct act gtt ata act aaa ggc atg aat gaa att aaa aca 672  
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 210 215 220

cta tat ata gca aaa aat cat tca ata gat ctt cat aca tta att ggt 720  
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 225 230 235 240

cca tca tgt ctt gga gat cta ata tta aca tgt aca aca gaa cat tca 768  
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 245 250 255

cgc aat atg gct ttt gga cta gaa ata gga aaa ggt aga aat ata aat 816  
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 260 265 270

aca tta ata gat cac aac cta aag ctt gtt gaa gga acc agt act gta 864  
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Lys Pro Leu Ile Ser Leu Ala	Lys Lys Leu Asn Val Glu Leu Pro Ile		
290	295 300		
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Cys Ile Ser Ile Tyr Asn Leu Leu His Glu Asn Ile Ser Leu Asp Lys			
305	310 315 320		
gcc ata tca aac ata tta tct tag			984
Ala Ile Ser Asn Ile Leu Ser			
325			

&lt;210&gt; 55

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Ehrlichia ruminantium (formerly Cowdria ruminantium)

&lt;400&gt; 55

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His Arg Asn Ile Thr His Ile Asn Thr Tyr Arg Lys Asn Leu Lys Tyr	
35	40 45

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50	55 60

Asp Glu Val Leu Ser Asp Asn Asn Thr Cys Ile Ile Leu Thr Ile Pro	
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Thr Gln Gln Leu Arg Thr Ile Cys Thr Gln Ile Gln His Lys Gln His	
85	90 95

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100	105 110

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115	120 125

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130

135

140

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145 150 155 160

Gly Glu Ser Leu Ile Glu Thr Ile Ser Asn Asp Val Leu Lys Ile Ile  
165 170 175

Tyr His Gln Asp Ile Ile Gly Val Gln Ile Gly Ala Ala Leu Lys Asn  
180 185 190

Ile Ile Ala Ile Ala Cys Gly Ile Ile Ala Gly Lys Asn Leu Gly Asn  
195 200 205

Asn Ala Val Ala Thr Val Ile Thr Lys Gly Met Asn Glu Ile Lys Thr  
210 215 220

Leu Tyr Ile Ala Lys Asn His Ser Ile Asp Leu His Thr Leu Ile Gly  
225 230 235 240

Pro Ser Cys Leu Gly Asp Leu Ile Leu Thr Cys Thr Thr Glu His Ser  
245 250 255

Arg Asn Met Ala Phe Gly Leu Glu Ile Gly Lys Gly Arg Asn Ile Asn  
260 265 270

Thr Leu Ile Asp His Asn Leu Lys Leu Val Glu Gly Thr Ser Thr Val  
275 280 285

Lys Pro Leu Ile Ser Leu Ala Lys Lys Leu Asn Val Glu Leu Pro Ile  
290 295 300

Cys Ile Ser Ile Tyr Asn Leu Leu His Glu Asn Ile Ser Leu Asp Lys  
305 310 315 320

Ala Ile Ser Asn Ile Leu Ser  
325

<210> 56

<211> 1416

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)



<220>  
 <221> misc\_feature  
 <222> (1)..(1416)  
 <223> Complement to SEQ ID NO:52, nucleotides 2467..3882  
 Hypothetical nitrogen assimilation regulatory protein  
 Product = "19hworf3"

<400> 56  
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 cattccaaca aattcagcag ttcgtgatac attacctcca aaacgagata actgagtttt 120  
 taaatactgt ctttcaaatt cttcagcagc tttacgtaat ggtacagaaa taacttttagc 180  
 acttaaaaca tcattaatag gcgaattaga tactatatct actggtaaact cttttgctgt 240  
 aatcatctcc ttaggagatt tcataattaa aatccattct ataacattac gtaattgtct 300  
 taagttacct ggccattcat atgactgcat tgctattaaa gcttcatcac ttaatacatg 360  
 agtacacaaa cctatttttt tacagatgct attcataaaa tacctacaca attccggtat 420  
 atctgtacaa tattotacta aagacggtag tctaattgga aggacattta atctataata 480  
 taaatcctca caaaacctac cagctttttac ttcactttca atatctttgg aagaagacac 540  
 aataattctc acatctatac taacaggaat cttactatct tccctatata tttttccctc 600  
 ctgtaataat ctgagtaatc ttaattgctg atcgatcggt aaatctgtta cttcatctat 660  
 aaataacgta ccatgatttg cttgctctat aattccaata tgaggaggta ctctatgaga 720  
 caatatatta ttactttcct cactacaaa tatattaacc aagtaattat tagctggtag 780  
 catagatgag tacatagata taaatggagt atcatacccc ttggattttt tatgtattag 840  
 cctagcaact acttcctttc caacacctgg cgaaccagta atgagtatac gactcgatgt 900  
 agtagctgct ttattaatca tactttctca attacgtata acaggggagt taccgactat 960  
 ttcataatcc tcaaatgctg atttcaactc atcattttct ctacgtaatc taccagactc 1020  
 tatagctctc tttacaacta actttaatct tccttctgta aaaggctttt ctatataatc 1080  
 ataagcacc atagtcagag actttacagc agtggcaata ttaccatgcc cactaatcat 1140  
 aataacaggc aaataaggat acctttcttt aagcttttcc agtacactta atccatcaat 1200  
 atcagatcct ctttaaccata tatccaataa tacaacatca ggctcttttt cataagccat 1260  
 cttgatcgcg gataaaccat caactgctaa tttagtgaca taattatcat cacttaatat 1320  
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caatctttcc ttggacattt caaaatcctg tgccat

1416

<210> 57

<211> 597

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> misc\_feature

<222> (1)..(597)

<223> Complement to SEQ ID NO:52, nucleotides 4154..>4750

Hypothetical cell division protein ftsQ

Product = "19hworf4i"

<400> 57

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aggtaat tttt atatttaaac cactagacaa aataatatcc caccaatgac tatcaacata 180

tgtgatagat gaaaccatac caccaacaag agtattatca ttgactactt cacgtataaa 240

atctagatga gttaacgcac catctccatg tattgaagtc aaatcatccc gtatattaca 300

attatcaaca ataatatgtc caaaactatc aatgatagaa tttttgttat catgatacca 360

atttgcaaaa gcagaatatt cttgaactgt tatctgtaaa gtatttggtta acagcctctt 420

aactgaggca tttttgatcc atggatgact agactctatt ttgtttctca aatcagccaa 480

aggcacaaaa aagatagacc ttgcatcaac aagtttacgt atttcatcag aacttacata 540

ttcattacca tcaatcaata ttttatcaac agtaaattcca caattgacta attgatc 597

<210> 58

<211> 4544

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 58

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ttatataatg caatcactga taatggagcc ggaggtctat catcttctat aggtgaaatg 120

ggaaataatg gatttaaagt agaactaaat aaagtattat taaaacataa aaacatgcta 180

ccttgggaaa tttgggtatc agaatcacia gaaagaatga cattagctat tcctccaagc 240

aaattcccaa tatttgaaaa aattatgaaa aagcatgatg ttgaaatcag tattattgga 300

acattcaata atacaaaaaa agcagtagta tcatataatg actccattat tatggatatg	360
gatataaact tcttacataa cggatatacca aaaactcatc taaaaacat accatgggtca	420
aacataatat cctcagtagt agacacatta cataataaac cactagacac tgagctaaat	480
gaaatgatgc aaagaatgaa tatatgtagt aaagaattta tctctacaca atatgatcat	540
gaagtacagg gaacatcagt cataaaacct atacaaggga aaggacgagt agatggagaa	600
gcaatagtta ttagaccaat actatcatca gaaaggggac tagtaaaatc acatggacta	660
ggatcaagct atggagaaat tagtacatac cacatggctg catgtgctat agatacagca	720
atacgttaatt atatagcaat cgggggaaat ttccatcact tagcattatt agataatttc	780
tgttggtgtg actctacaaa tccaaaaaga ttatggcaat taaaaaatgc tgcccaagca	840
tgttatgaat acgcaaaaat tttcaaaaca cttttcattt ctggaaaaga tagcatgttc	900
aatgatttta aagggtataa caataaagga gaacctatta acatttctgc tctccttca	960
cttttaattt ctacagtagg aataatagaa aatattcaca atgccataac acttgatgta	1020
aaaaatccag gagatttaat atacatatta ggtgtgacat atgatgaact tggaagggtcc	1080
gaataccaaa aatatagcgg attaggaaat aataatgttc cacaagtacg tgctaaacat	1140
gcaaaaaaac tatacaagtt atatagcaat gcagttaata caaatattat agcatctgca	1200
attgcattaa acctaggggg gctaattata ggtttaataa aatcactaat tggaggagaa	1260
ctgggagcaa aaattgactt atcactagta ccaacacata atattgaaga taataacata	1320
aaagagaaag taatcctatt ttcagaatca caaagtagaa ttttagtaac aatagctcca	1380
cataataaac aaaaatttga aactattttt aaagacatag cacatgcaa cataggtata	1440
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atttagttag taattaattt tacttttatt accttaatag tcttagttga tatataaatt	1620
ttatatacta tggatagata ttatgcatta ttgaaaatat ctataatgtt aatccaaatg	1680
aactgaaaca tagttataag aaattcacca atatgaaaat acgagtaata aaactattgt	1740
ttttattcta ctacattaat aattgaacct tgatccaatc ttggtatatt acagcatcgt	1800
gattatcaaa aacatgtata cactaataaa attataaaaa actcaatatt ttaataatat	1860
atatgtatac ataagaacaa tatattttttt acaactcaat tattaagcca tacagattat	1920
agtttcttgt ttaataaata agtaaaaaata atacaaaatc tatttttcta atttatttaa	1980

aacgaattta tatactggac ctactgtata ctatataagg aatataaaaa tacacttata 2040  
 atcagattag aaatttatca taatatttca atatatttgt taatttcatt atctaattga 2100  
 tatctatata taatgtcttc tccttactaa ttataacacc ttatttgaat actaaaatca 2160  
 tgtaatactt ttctcaactt aaaaattgaa atgacaaaaa atctattcta taattcatat 2220  
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 agtactagca ttaggtagta attgtggcag tatgttattg aatattaaat ctgctataaa 2340  
 tatgttatct ttatataaca aaacatattc ttatatctat aaaagtatgg cactattacc 2400  
 agaaaattct agtagtgatt gggatactcc ttttctgaat atggtagtat caggttatac 2460  
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 aatggtatat atatcaggaa atacttctca atctacgtaa gtcaacctaa taaagcagtt 3000  
 atatattata actcagtatt tatatataat atttagagta ttaacagtac tatcataagt 3060  
 atatgtatag tatagcaagt tatattagat tatattttaa aatacataac cagatcataa 3120  
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 caatccatat ttattactta tcatattatt cagaaattat tactttcctt cactgattcc 3240  
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 aacactagaa cgtttcattt ttataaccta actctacata accaacaatcc tttaattaat 3600

atcaacattg atagatcact ttttaataaa tacaataaaa ttgtcggata ttaatactat 3660  
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 tacaatagca ctttttatct atacttaact atctaacta atatgccaca gcagtactat 3960  
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 agtggttaatt tttccaccac aaccagtaaa acataaatca taatcactcc tacataatct 4080  
 atcacatca tttaccttac ataaacttac aggtttcaca ggaactacag attttatacc 4140  
 agtccaaaa gattttgaag tactactact ttgtacttca tgcttaaaaag atcctgaaga 4200  
 aaaactcata tcagttttta ctcgttgctc agtatcacac acattaaatt gcatatcaca 4260  
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 acatggatta ttactatctt ctttatcatc attaccttta ctgatagtat tgtttattat 4380  
 actaataaat ggattacgac gagtttgctc atcaatcatt ttctctgcta atcgacaatc 4440  
 tgtaactta acctgacatt gcctatagca atcattctta ttgtaactac attgaagtat 4500  
 acatgctttg ccaacttcat tgtctggagc ttcatagttt gatc 4544

<210> 59

<211> 1566

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> CDS

<222> (1)..(1566)

<223> Corresponds to SEQ ID NO:58, nucleotides <1..1566  
 Hypothetical phosphoribosylformylglycinamide synthase  
 Product = "21hworfli"

<400> 59

gat cca att aca caa aag aaa ttg tct gat gct atc att aaa gaa gca 48  
 Asp Pro Ile Thr Gln Lys Lys Leu Ser Asp Ala Ile Ile Lys Glu Ala  
 1 5 10 15

aga gat tta aac tta tat aat gca atc act gat aat gga gcc gga ggt 96  
 Arg Asp Leu Asn Leu Tyr Asn Ala Ile Thr Asp Asn Gly Ala Gly Gly  
 20 25 30

cta tca tct tct ata ggt gaa atg gga aat aat gga ttt aaa gta gaa 144  
 Leu Ser Ser Ser Ile Gly Glu Met Gly Asn Asn Gly Phe Lys Val Glu  
 35 40 45

cta aat aaa gta tta tta aaa cat aaa aac atg cta cct tgg gaa att 192  
 Leu Asn Lys Val Leu Leu Lys His Lys Asn Met Leu Pro Trp Glu Ile  
 50 55 60

tgg gta tca gaa tca caa gaa aga atg aca tta gct att cct cca agc 240  
 Trp Val Ser Glu Ser Gln Glu Arg Met Thr Leu Ala Ile Pro Pro Ser  
 65 70 75 80

aaa ttc cca ata ttt gaa aaa att atg aaa aag cat gat gtt gaa atc 288  
 Lys Phe Pro Ile Phe Glu Lys Ile Met Lys Lys His Asp Val Glu Ile  
 85 90 95

agt att att gga aca ttc aat aat aca aaa aaa gca gta gta tca tat 336  
 Ser Ile Ile Gly Thr Phe Asn Asn Thr Lys Lys Ala Val Val Ser Tyr  
 100 105 110

aat gac tcc att att atg gat atg gat ata aac ttc tta cat aac ggt 384  
 Asn Asp Ser Ile Ile Met Asp Met Asp Ile Asn Phe Leu His Asn Gly  
 115 120 125

ata cca aaa act cat cta aaa acc ata cca tgg tca aac ata ata tcc 432  
 Ile Pro Lys Thr His Leu Lys Thr Ile Pro Trp Ser Asn Ile Ile Ser  
 130 135 140

tca gta gta gac aca tta cat aat aaa cca cta gac act gag cta aat 480  
 Ser Val Val Asp Thr Leu His Asn Lys Pro Leu Asp Thr Glu Leu Asn  
 145 150 155 160

gaa atg atg caa aga atg aat ata tgt agt aaa gaa ttt atc tct aca 528  
 Glu Met Met Gln Arg Met Asn Ile Cys Ser Lys Glu Phe Ile Ser Thr  
 165 170 175

caa tat gat cat gaa gta cag gga aca tca gtc ata aaa cct ata caa 576  
 Gln Tyr Asp His Glu Val Gln Gly Thr Ser Val Ile Lys Pro Ile Gln  
 180 185 190

ggg aaa gga cga gta gat gga gaa gca ata gtt att aga cca ata cta 624  
 Gly Lys Gly Arg Val Asp Gly Glu Ala Ile Val Ile Arg Pro Ile Leu  
 195 200 205

tca tca gaa agg gga cta gta aaa tca cat gga cta gga tca agc tat 672  
 Ser Ser Glu Arg Gly Leu Val Lys Ser His Gly Leu Gly Ser Ser Tyr  
 210 215 220

gga gaa att agt aca tac cac atg gct gca tgt gct ata gat aca gca 720  
 Gly Glu Ile Ser Thr Tyr His Met Ala Ala Cys Ala Ile Asp Thr Ala  
 225 230 235 240

ata cgt aat tat ata gca atc ggg gga aat ttc cat cac tta gca tta 768  
 Ile Arg Asn Tyr Ile Ala Ile Gly Gly Asn Phe His His Leu Ala Leu  
 245 250 255

tta gat aat ttc tgt tgg tgt gac tct aca aat cca aaa aga tta tgg Leu Asp Asn Phe Cys Trp Cys Asp Ser Thr Asn Pro Lys Arg Leu Trp 260 265 270	816
caa tta aaa aat gct gcc caa gca tgt tat gaa tac gca aaa att ttc Gln Leu Lys Asn Ala Ala Gln Ala Cys Tyr Glu Tyr Ala Lys Ile Phe 275 280 285	864
aaa aca cct ttc att tct gga aaa gat agc atg ttc aat gat ttt aaa Lys Thr Pro Phe Ile Ser Gly Lys Asp Ser Met Phe Asn Asp Phe Lys 290 295 300	912
ggg tat aac aat aaa gga gaa cct att aac att tct gct cct cct tca Gly Tyr Asn Asn Lys Gly Glu Pro Ile Asn Ile Ser Ala Pro Pro Ser 305 310 315 320	960
ctt tta att tct aca gta gga ata ata gaa aat att cac aat gcc ata Leu Leu Ile Ser Thr Val Gly Ile Ile Glu Asn Ile His Asn Ala Ile 325 330 335	1008
aca ctt gat gta aaa aat cca gga gat tta ata tac ata tta ggt gtg Thr Leu Asp Val Lys Asn Pro Gly Asp Leu Ile Tyr Ile Leu Gly Val 340 345 350	1056
aca tat gat gaa ctt gga agg tcc gaa tac caa aaa tat agc gga tta Thr Tyr Asp Glu Leu Gly Arg Ser Glu Tyr Gln Lys Tyr Ser Gly Leu 355 360 365	1104
gga aat aat aat gtt cca caa gta cgt gct aaa cat gca aaa aaa cta Gly Asn Asn Asn Val Pro Gln Val Arg Ala Lys His Ala Lys Lys Leu 370 375 380	1152
tac aag tta tat agc aat gca gtt aat aca aat att ata gca tct gca Tyr Lys Leu Tyr Ser Asn Ala Val Asn Thr Asn Ile Ile Ala Ser Ala 385 390 395 400	1200
att gca tta aac cta ggg ggg cta att ata ggt tta ata aaa tca cta Ile Ala Leu Asn Leu Gly Gly Leu Ile Ile Gly Leu Ile Lys Ser Leu 405 410 415	1248
att gga gga gaa ctg gga gca aaa att gac tta tca cta gta cca aca Ile Gly Gly Glu Leu Gly Ala Lys Ile Asp Leu Ser Leu Val Pro Thr 420 425 430	1296
cat aat att gaa gat aat aac ata aaa gag aaa gta atc cta ttt tca His Asn Ile Glu Asp Asn Asn Ile Lys Glu Lys Val Ile Leu Phe Ser 435 440 445	1344
gaa tca caa agt aga att tta gta aca ata gct cca cat aat aaa caa Glu Ser Gln Ser Arg Ile Leu Val Thr Ile Ala Pro His Asn Lys Gln 450 455 460	1392
aaa ttt gaa act att ttt aaa gac ata gca cat gca aac ata ggt ata Lys Phe Glu Thr Ile Phe Lys Asp Ile Ala His Ala Asn Ile Gly Ile	1440

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<210> 60
<211> 521
<212> PRT
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)
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<400> 60
Asp Pro Ile Thr Gln Lys Lys Leu Ser Asp Ala Ile Ile Lys Glu Ala
1           5           10           15
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Arg Asp Leu Asn Leu Tyr Asn Ala Ile Thr Asp Asn Gly Ala Gly Gly  
20 25 30

Leu Ser Ser Ser Ile Gly Glu Met Gly Asn Asn Gly Phe Lys Val Glu  
35 40 45

Leu Asn Lys Val Leu Leu Lys His Lys Asn Met Leu Pro Trp Glu Ile  
50 55 60

Trp Val Ser Glu Ser Gln Glu Arg Met Thr Leu Ala Ile Pro Pro Ser  
65 70 75 80

Lys Phe Pro Ile Phe Glu Lys Ile Met Lys Lys His Asp Val Glu Ile  
85 90 95

Ser Ile Ile Gly Thr Phe Asn Asn Thr Lys Lys Ala Val Val Ser Tyr  
100 105 110

Asn Asp Ser Ile Ile Met Asp Met Asp Ile Asn Phe Leu His Asn Gly  
115 120 125

Ile Pro Lys Thr His Leu Lys Thr Ile Pro Trp Ser Asn Ile Ile Ser

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130

135

140

Ser Val Val Asp Thr Leu His Asn Lys Pro Leu Asp Thr Glu Leu Asn  
145 150 155 160

Glu Met Met Gln Arg Met Asn Ile Cys Ser Lys Glu Phe Ile Ser Thr  
165 170 175

Gln Tyr Asp His Glu Val Gln Gly Thr Ser Val Ile Lys Pro Ile Gln  
180 185 190

Gly Lys Gly Arg Val Asp Gly Glu Ala Ile Val Ile Arg Pro Ile Leu  
195 200 205

Ser Ser Glu Arg Gly Leu Val Lys Ser His Gly Leu Gly Ser Ser Tyr  
210 215 220

Gly Glu Ile Ser Thr Tyr His Met Ala Ala Cys Ala Ile Asp Thr Ala  
225 230 235 240

Ile Arg Asn Tyr Ile Ala Ile Gly Gly Asn Phe His His Leu Ala Leu  
245 250 255

Leu Asp Asn Phe Cys Trp Cys Asp Ser Thr Asn Pro Lys Arg Leu Trp  
260 265 270

Gln Leu Lys Asn Ala Ala Gln Ala Cys Tyr Glu Tyr Ala Lys Ile Phe  
275 280 285

Lys Thr Pro Phe Ile Ser Gly Lys Asp Ser Met Phe Asn Asp Phe Lys  
290 295 300

Gly Tyr Asn Asn Lys Gly Glu Pro Ile Asn Ile Ser Ala Pro Pro Ser  
305 310 315 320

Leu Leu Ile Ser Thr Val Gly Ile Ile Glu Asn Ile His Asn Ala Ile  
325 330 335

Thr Leu Asp Val Lys Asn Pro Gly Asp Leu Ile Tyr Ile Leu Gly Val  
340 345 350

Thr Tyr Asp Glu Leu Gly Arg Ser Glu Tyr Gln Lys Tyr Ser Gly Leu  
355 360 365

Gly Asn Asn Asn Val Pro Gln Val Arg Ala Lys His Ala Lys Lys Leu  
370 375 380

Tyr Lys Leu Tyr Ser Asn Ala Val Asn Thr Asn Ile Ile Ala Ser Ala  
385 390 395 400

Ile Ala Leu Asn Leu Gly Gly Leu Ile Ile Gly Leu Ile Lys Ser Leu  
405 410 415

Ile Gly Gly Glu Leu Gly Ala Lys Ile Asp Leu Ser Leu Val Pro Thr  
420 425 430

His Asn Ile Glu Asp Asn Asn Ile Lys Glu Lys Val Ile Leu Phe Ser  
435 440 445

Glu Ser Gln Ser Arg Ile Leu Val Thr Ile Ala Pro His Asn Lys Gln  
450 455 460

Lys Phe Glu Thr Ile Phe Lys Asp Ile Ala His Ala Asn Ile Gly Ile  
465 470 475 480

Ile Ser Asp Thr Asn Thr Leu Ile Ile Asn Asn Met His Ile Ile Asn  
485 490 495

Leu Asn Thr Leu Lys His Ser Tyr Lys Lys Phe Ser Asn Met Lys Ile  
500 505 510

Gln Ala Tyr Ala Asp Ala Glu Tyr Ile  
515 520

<210> 61  
<211> 525  
<212> DNA  
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
<221> CDS  
<222> (1)..(525)  
<223> Corresponds to SEQ ID NO:58, nucleotides 2252..2776  
Hypothetical folic acid synthesis protein  
Product = "21hworf2"

<400> 61  
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 1 5 10 15  
  
 aat tgt ggc agt atg tta ttg aat att aaa tct gct ata aat atg tta 96  
 Asn Cys Gly Ser Met Leu Leu Asn Ile Lys Ser Ala Ile Asn Met Leu  
 20 25 30  
  
 tct tta tat aac aaa aca tat tct tat atc tat aaa agt atg gca cta 144  
 Ser Leu Tyr Asn Lys Thr Tyr Ser Tyr Ile Tyr Lys Ser Met Ala Leu  
 35 40 45  
  
 tta cca gaa aat tct agt agt gat tgg gat act cct ttt ctg aat atg 192  
 Leu Pro Glu Asn Ser Ser Ser Asp Trp Asp Thr Pro Phe Leu Asn Met  
 50 55 60  
  
 gta gta tca ggt tat aca aat ctt tca cca aat ctt atg tta gaa aga 240  
 Val Val Ser Gly Tyr Thr Asn Leu Ser Pro Asn Leu Met Leu Glu Arg  
 65 70 75 80  
  
 gtt aaa tac att gaa aaa aaa ata ggc agg ttt aat aat gaa tac tgg 288  
 Val Lys Tyr Ile Glu Lys Lys Ile Gly Arg Phe Asn Asn Glu Tyr Trp  
 85 90 95  
  
 tca cct aga tgt ata gat att gac att atc tta tgg gga gat aaa gtc 336  
 Ser Pro Arg Cys Ile Asp Ile Asp Ile Ile Leu Trp Gly Asp Lys Val  
 100 105 110  
  
 tta gac tca caa act tta tct att cct cat aag cat atg caa gat aga 384  
 Leu Asp Ser Gln Thr Leu Ser Ile Pro His Lys His Met Gln Asp Arg  
 115 120 125  
  
 gat ttt gta ctt gta cca ctc tgt gat att cac gca aga ttt cct cat 432  
 Asp Phe Val Leu Val Pro Leu Cys Asp Ile His Ala Arg Phe Pro His  
 130 135 140  
  
 cca gta tca aag cta tca att gaagaa ata gtt ctc aat cta cat gag 480  
 Pro Val Ser Lys Leu Ser Ile Glu Glu Ile Val Leu Asn Leu His Glu  
 145 150 155 160  
  
 atc aat tta ata aag cag tca tat att ata act caa tat tta tag 525  
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 165 170

<210> 62

<211> 174

<212> PRT

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 62

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1 5 10 15

Asn Cys Gly Ser Met Leu Leu Asn Ile Lys Ser Ala Ile Asn Met Leu  
20 25 30

Ser Leu Tyr Asn Lys Thr Tyr Ser Tyr Ile Tyr Lys Ser Met Ala Leu  
35 40 45

Leu Pro Glu Asn Ser Ser Ser Asp Trp Asp Thr Pro Phe Leu Asn Met  
50 55 60

Val Val Ser Gly Tyr Thr Asn Leu Ser Pro Asn Leu Met Leu Glu Arg  
65 70 75 80

Val Lys Tyr Ile Glu Lys Lys Ile Gly Arg Phe Asn Asn Glu Tyr Trp  
85 90 95

Ser Pro Arg Cys Ile Asp Ile Asp Ile Ile Leu Trp Gly Asp Lys Val  
100 105 110

Leu Asp Ser Gln Thr Leu Ser Ile Pro His Lys His Met Gln Asp Arg  
115 120 125

Asp Phe Val Leu Val Pro Leu Cys Asp Ile His Ala Arg Phe Pro His  
130 135 140

Pro Val Ser Lys Leu Ser Ile Glu Glu Ile Val Leu Asn Leu His Glu  
145 150 155 160

Ile Asn Leu Ile Lys Gln Ser Tyr Ile Ile Thr Gln Tyr Leu  
165 170

<210> 63  
<211> 560  
<212> DNA  
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)  
  
<220>  
<221> misc\_feature  
<222> (1)..(560)  
<223> Complement to SEQ ID NO:58, nucleotides 3985..>4544  
Product = "21hworf3i"

**THE**

[illegible]

**THE**

[illegible][illegible]

**THE**

[illegible][illegible]

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taatatatca cagcatatgt gaaatattgg atgatatttc aaaaaaagct catgataaga	960
atcttcataa cttaaaatca aacccttact tagtaatact acagataata ttaatagact	1020
tagtattctc aatagattca atactcactg ctataggaat tacatataac atttttataa	1080
tccaactagt atttataata tccataatac ttacaatctt attttcaaag catatcatag	1140
aagctattac aaaatacagt aacatcaaaa ctatagctgt catgtttgtc ttaatattag	1200
gtatcatact agtactagat ggaatacata ttaaaatata ccataattat ttatatttta	1260
cctttatctt ttctagcctc gttgaaataa taaatattat aaaaaagtca agcaatagcc	1320
taatacagta aaattaataa gcataatagg taatttattt aattcattat acaatgatat	1380
ctctaaaaat ttatacacia attgtaaaga gacacatata acataaatta aaatatgtta	1440
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aattagctct aatattttac tttaaatatt acaattaata ttgttaccia tataattata	1560
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agtttctaag tagacatcaa tatgtctaaa acagaaatgg aatataaatc tttttttata	1740
caaagaatac tacaactata gtggttaagt cagtttacat tgctaaagat tgttattttt	1800
acaattaaat gcctttaatt atatatatta ccgtatatgg ttattattat tttacagtat	1860
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agaagtacaa tatattctgt atttaacttc ttttaaattt gatattctaa taaattgata	1980
aaagtatatt atacttaaac tttgtgatac atatcctttg cctaattata aaaaatgatt	2040
ttttattgaa atagttaata tgttattcaa aatatttgaa taacatgtaa gaatgattgt	2100
atattaaaga tatacaatca ttagttcata aagtatattc gtacctttaa tgggttaataa	2160
tataatgtat ttacatatta gatatcattt ataataacat aaaaaaatgc ttcaataata	2220
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ttataactta acataatagc aataatatta accaactctc cacagaaaaa cttaactata	2340
cacagttact gcttgattac tattgattac ttttttggtt caatacacat aacattttac	2400
taattaactg ataactctag cgttgcgaaa ttatcataaa tatcattatt taatataaca	2460

agaataacac ataataatat taacaatgta cactagaaat aataactaac aagatataaa 2520  
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atgaagtttt tccatgatca acatgtccca taacagtaac aactggtgct ctaggaatca 4380  
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taaagtgtatg attgaacgct tctactataa tagaagcttg atc 4483

<210> 65  
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<212> DNA  
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)  
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<221> CDS  
<222> (1)..(708)  
<223> Corresponds to SEQ ID NO:64, nucleotides 624..1331  
Hypothetical transmembrane protein  
Product = "23hworf1"

<400> 65  
atg ttt gaa aac gat ata ttc aag ttt ttc aca cta cta cta tta gaa 48  
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1 5 10 15  
atc att tta ggt ata gat aat gtg att ttt ata tca ctt gcc gtt ata 96  
Ile Ile Leu Gly Ile Asp Asn Val Ile Phe Ile Ser Leu Ala Val Ile  
20 25 30  
aaa gta cca gat acc tta cgc aac aaa gta aga tat ata gga cta gca 144  
Lys Val Pro Asp Thr Leu Arg Asn Lys Val Arg Tyr Ile Gly Leu Ala  
35 40 45  
tta gca tta ata atg cga ctc gtt gca tta cag aca gca tcg ata tta 192  
Leu Ala Leu Ile Met Arg Leu Val Ala Leu Gln Thr Ala Ser Ile Leu  
50 55 60  
ttg tca cta aat aaa cca gta ata ttc cta gca caa ctt cat tta tca 240  
Leu Ser Leu Asn Lys Pro Val Ile Phe Leu Ala Gln Leu His Leu Ser  
65 70 75 80  
ccc aat aac tta ttt atg ata ttt gga gga gta ttc tta ata tat cac 288  
Pro Asn Asn Leu Phe Met Ile Phe Gly Gly Val Phe Leu Ile Tyr His  
85 90 95  
agc ata tgt gaa ata ttg gat gat att tca aaa aaa gct cat gat aag 336  
Ser Ile Cys Glu Ile Leu Asp Asp Ile Ser Lys Lys Ala His Asp Lys



100	105	110	
aat ctt cat aac tta aaa tca aac cct tac tta gta ata cta cag ata			384
Asn Leu His Asn Leu Lys Ser Asn Pro Tyr Leu Val Ile Leu Gln Ile			
115	120	125	
ata tta ata gac tta gta ttc tca ata gat tca ata ctc act gct ata			432
Ile Leu Ile Asp Leu Val Phe Ser Ile Asp Ser Ile Leu Thr Ala Ile			
130	135	140	
gga att aca tat aac att ttt ata atc caa cta gta ttt ata ata tcc			480
Gly Ile Thr Tyr Asn Ile Phe Ile Ile Gln Leu Val Phe Ile Ile Ser			
145	150	155	160
ata ata ctt aca atc tta ttt tca aag cat atc ata gaa gct att aca			528
Ile Ile Leu Thr Ile Leu Phe Ser Lys His Ile Ile Glu Ala Ile Thr			
165	170	175	
aaa tac agt aac atc aaa act ata gct gtc atg ttt gtc tta ata tta			576
Lys Tyr Ser Asn Ile Lys Thr Ile Ala Val Met Phe Val Leu Ile Leu			
180	185	190	
ggt atc ata cta gta cta gat gga ata cat att aaa ata tcc cat aat			624
Gly Ile Ile Leu Val Leu Asp Gly Ile His Ile Lys Ile Ser His Asn			
195	200	205	
tat tta tat ttt acc ttt atc ttt tct agc ctc gtt gaa ata ata aat			672
Tyr Leu Tyr Phe Thr Phe Ile Phe Ser Ser Leu Val Glu Ile Ile Asn			
210	215	220	
att ata aaa aag tca agc aat agc cta ata cag taa			708
Ile Ile Lys Lys Ser Ser Asn Ser Leu Ile Gln			
225	230	235	

&lt;210&gt; 66

&lt;211&gt; 235

&lt;212&gt; PRT

&lt;213&gt; Ehrlichia ruminantium (formerly Cowdria ruminantium)

&lt;400&gt; 66

Met Phe Glu Asn Asp Ile Phe Lys Phe Phe Thr Leu Leu Leu Glu
1 5 10 15

Ile Ile Leu Gly Ile Asp Asn Val Ile Phe Ile Ser Leu Ala Val Ile
20 25 30

Lys Val Pro Asp Thr Leu Arg Asn Lys Val Arg Tyr Ile Gly Leu Ala
35 40 45

Leu Ala Leu Ile Met Arg Leu Val Ala Leu Gln Thr Ala Ser Ile Leu
---

50

55

60

Leu Ser Leu Asn Lys Pro Val Ile Phe Leu Ala Gln Leu His Leu Ser  
65 70 75 80

Pro Asn Asn Leu Phe Met Ile Phe Gly Gly Val Phe Leu Ile Tyr His  
85 90 95

Ser Ile Cys Glu Ile Leu Asp Asp Ile Ser Lys Lys Ala His Asp Lys  
100 105 110

Asn Leu His Asn Leu Lys Ser Asn Pro Tyr Leu Val Ile Leu Gln Ile  
115 120 125

Ile Leu Ile Asp Leu Val Phe Ser Ile Asp Ser Ile Leu Thr Ala Ile  
130 135 140

Gly Ile Thr Tyr Asn Ile Phe Ile Ile Gln Leu Val Phe Ile Ile Ser  
145 150 155 160

Ile Ile Leu Thr Ile Leu Phe Ser Lys His Ile Ile Glu Ala Ile Thr  
165 170 175

Lys Tyr Ser Asn Ile Lys Thr Ile Ala Val Met Phe Val Leu Ile Leu  
180 185 190

Gly Ile Ile Leu Val Leu Asp Gly Ile His Ile Lys Ile Ser His Asn  
195 200 205

Tyr Leu Tyr Phe Thr Phe Ile Phe Ser Ser Leu Val Glu Ile Ile Asn  
210 215 220

Ile Ile Lys Lys Ser Ser Asn Ser Leu Ile Gln  
225 230 235

<210> 67

<211> 348

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> misc\_feature

<222> (1)..(348)

<223> Complement to SEQ ID NO:64, nucleotides 2526..2873  
Hypothetical ribosome-binding factor A  
Product = "23hworf2"

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aaaatataat ttcggtacat atctaagatc tacatatgaa aatatagcct ttcttatttaa 120  
aaatgaaaca tcgttttagtt cttttacaag attttcttta tctggatgat catcggaat 180  
tacaacaaat acagtagcat tttttacatc ttactcact tctacttttag atacattaac 240  
tatactacaa cctattgaat aaatatcatg tatcaatact ctogatattg ctctgcttaa 300  
tactgaagca acctttaaat ttctaaaact ctcagattta taaatcat 348

<210> 68  
<211> 1614  
<212> DNA  
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
<221> misc\_feature  
<222> (1)..(1614)  
<223> Complement to SEQ ID NO:64, nucleotides 2870..>4483  
Hypothetical translation initiation factor IF-2  
Product = "23hworf3i"

<400> 68  
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tacatcatct ttaaactgac gtaagacttt aatcttacct tcatgcataa tattattatt 180  
acgaactaac ttaactaatg cacctttttt taccaaacca cttgttacat aacaccaag 240  
tacactaccg ttattaccta cagaaaacac ttttctcaca gacaaagtac ctatctgtac 300  
ctcttgtttc aatggcctca acataccagt tagtatcttc ttaatatcat ctattatatt 360  
gtatataaca aaataatgct ttatttcgat atttttctgt tttgccatt cttttacttg 420  
cgtatccgtt ttaacattaa atgctaaaat tattgaattt gatgtttccg ctaataaaac 480  
atctgacttt gtaatatcc ctacaccttt atatagaata ttaactcgta tatctttatg 540  
agtaatttta ccaattgaat aacatatagc ttctatagaa ccataacat cacacttta 600  
gataacgttc aactcatcaa ccatatcata aagcaatata ttactcttat cgattgctgg 660

ctgtttactc aattccacat ttagtaaate ttgcctataa ttaattaatt cacgtgcttg 720  
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 taccttaatt ggcattgaag gaatagcaac tttttcactc ccaccatctg cattaaacat 840  
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 tactgtacca gatgccttag tattatatac agcttttaac tctaacaaat ctgcaatcaa 1020  
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 aataacatca cctcctaaac tttctgctac cactccatgc tgtaataaag cattagtaat 1140  
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 tctaggaate aattccatat tattaccatc agaataataa tcattttcta atttagcatt 1560  
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<210> 69

<211> 3829

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 69

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 cacttagaat tagcagcaga cattgctcaa gcttttaaca caaaatacaa tacgcaatac 300  
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 ggtaaaaaga aaatgagtaa atctgatgta tcagattatt cacgaattaa tttagaagat 420  
 agtaacgact taattgctca aaaaattaac aaagcaacca ctgactctat tgtaggtttt 480

gactttacaa gtttaaacia taggcctgca gtaaagaatc ttgttaatat ttatgctaca	540
ctttcaaata ttagtataga acaaacatgt actaacattg caagcttcac tactaaacia	600
tttaaagaag aactaacaga attaattatt aataacattg caccaatacg aaaaaatta	660
agagagttat tagaagacat agaatatatta cgaagcatat taatgacagg aaataacaag	720
gctgcatcta ttgcacataa gcacataata gaaattaaaa agattgcagg atattggtaa	780
taattataca aaattcatta atactcaaag tcatatcctt tggttattat tgtatgtgtc	840
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tacaatatat taatatcaac agtctcagta tgttgagaga ttcatatatta ttttaattaaa	960
ctataatctt cttgactatc atctttatat attaggccat tttatataaa aaaaaagaaa	1020
agaaatccta ctcattaata tctaaatatt aaaagagcta ctacaaaata actaccataa	1080
tacatctata gcaaaataaa gaatccatag catcaaaata tctatactaa attcactatc	1140
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gtccataaaa tacacattct cacaagagtt agtacacagt aaagagaaaa aaaagttagc	1440
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ttaatgctct ataatcctat ttatacccta gtgtaaaatc taaataatat ttttcttact	1860
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aacaatatct catttatattt atttttcaaa aataaactat aagcaattat taccatctaa	1980
gcttatctaa atataattta tctatactat accattataa atctgattac tataaagatt	2040
gaactatagt catccaaagg tttatacttg cttaatttta ctttacacia aacaacaatt	2100
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 gtacaacttt gtgtagtaaa taagtcacac tacttttcaa tctctacaat tacgaagata 3540  
 cagatgtaaa ttcgctatct tgagaagccg tatcagtaac agatactaaa ttagcactta 3600  
 cacaatcaac attatgattg tggcaatctt ctgttaatgg atgaagatta agagaaaaat 3660  
 tagaaccttg ttgtaaaaac tctgaaaaag gttccattaa atttactaca aaagaagctt 3720  
 gtaagctgtg atttaataca tcaagtgcac tatgttgacc agtaacacca tgaaaatctg 3780

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3829

<210> 70  
 <211> 780  
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 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)  
 <220>  
 <221> CDS  
 <222> (1)..(780)  
 <223> Corresponds to SEQ ID NO:69, nucleotides <1..780  
 Hypothetical tryptophanyl-tRNA ligase  
 Product = "26hworfli"

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 1 5 10 15  
 aca gag tta cta tgg ata ttc agt tgc att act tca aca ggt caa cta 96  
 Thr Glu Leu Leu Trp Ile Phe Ser Cys Ile Thr Ser Thr Gly Gln Leu  
 20 25 30  
 aat aga atg act caa ttt aaa gaa aaa agc cgc aat aaa gtt tct aca 144  
 Asn Arg Met Thr Gln Phe Lys Glu Lys Ser Arg Asn Lys Val Ser Thr  
 35 40 45  
 gct tct tta gga ttg tac agc tat cct gta tta atg gca gct gat ata 192  
 Ala Ser Leu Gly Leu Tyr Ser Tyr Pro Val Leu Met Ala Ala Asp Ile  
 50 55 60  
 tta ctt tac caa gca aat ata gta cct gta ggc att gat caa aaa caa 240  
 Leu Leu Tyr Gln Ala Asn Ile Val Pro Val Gly Ile Asp Gln Lys Gln  
 65 70 75 80  
 cac tta gaa tta gca cga gac att gct caa gct ttt aac aca aaa tac 288  
 His Leu Glu Leu Ala Arg Asp Ile Ala Gln Ala Phe Asn Thr Lys Tyr  
 85 90 95  
 aat acg caa tac ttt caa ctg cca gaa cca tta att gta cag gaa tca 336  
 Asn Thr Gln Tyr Phe Gln Leu Pro Glu Pro Leu Ile Val Gln Glu Ser  
 100 105 110  
 gca aaa att atg agt tta aga gac ggt aaa aag aaa atg agt aaa tct 384  
 Ala Lys Ile Met Ser Leu Arg Asp Gly Lys Lys Lys Met Ser Lys Ser  
 115 120 125  
 gat gta tca gat tat tca cga att aat tta gaa gat agt aac gac tta 432  
 Asp Val Ser Asp Tyr Ser Arg Ile Asn Leu Glu Asp Ser Asn Asp Leu  
 130 135 140  
 att gct caa aaa att aac aaa gca acc act gac tct att gta ggt ttt 480  
 Ile Ala Gln Lys Ile Asn Lys Ala Thr Thr Asp Ser Ile Val Gly Phe

[illegible]

<400> 71

Leu Leu Tyr Gln Ala Asn Ile Val Pro Val Gly Ile Asp Gln Lys Gln



Gly Tyr Trp

T:\Sequences\UF\UF-299XC1\As-Filed-Seg-List.txt/DNB/jaj

<220>  
 <221> misc\_feature  
 <222> (1)..(1056)  
 <223> Complement to SEQ ID NO:69, nucleotides 2361..3416  
 Similar to cell surface mucin, protein contains 9-mer tandem repe  
 at  
 Product = "26hworf2"

<400> 72  
 ttagatgcc a gtaaatactc tttcaccact acgaccacca aatgtaaadc cttttgctac 60  
 ttctgggcta cttgttaca ctgacccctc tgggctactt gttacaactg atccttcttg 120  
 gctacttggt acaactgac cttctgggct acttggtaca actgacccct ctgggctact 180  
 tgttacaact gatccctctg ggctacttgt tacaactgat ccttctgggc tacttggtac 240  
 aactgaccc tctgggctac ttgttacaac tgatccctct gggctacttg ttacaactga 300  
 tccttctggg ctacttggtt caactgatcc ttctgggcta cttgttaca ctgacccctc 360  
 tgggctactt gttacaactg atccttcttg gctacttggt acaactgac cttctgggct 420  
 acttggtaca actgacccct ctgggctact tgttacaact gatccctctg ggctacttgt 480  
 tacaactgat ccttctgggc tacttggtac aactgaccc tctgggctac ttgttacaac 540  
 tgatccctct gggctacttg ttacaactga tccttctggg ctacttggtt caactgatcc 600  
 ttctgggcta cttgttacag ctgctccctc tgggctatct gttacagttg tatcaacacc 660  
 tgagatcacc ttatcatagc acacatttaa tggatgaaga ttaagagaaa aattagaacc 720  
 ttgttgtaaa aactctgaaa aagggtccat taaatttact aaaaagaag cttgtaagct 780  
 gtggtttaat acatcaagtg caatatgttt accagtaaca ccatgaaaat ctgaaagtac 840  
 gtgaccatta ctgtaaaaca taacatgata ttgccatga tgattttcat gaccttcttc 900  
 atgctcatga ggatgatagc caatctccat tgtaatatca ccatttgaaa cagagaattg 960  
 attattacta tagatactta aatcatttcc aaaatcaata ttgtcaattc ttgttggtta 1020  
 atgaagcata caatcttctg ctgttgaatg aaccat 1056

<210> 73  
 <211> 300  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
 <221> misc\_feature

<222> (1)..(300)

<223> Complement to SEQ ID NO:69, nucleotides 3530..>3829

Similar to 26hworf2

Product = "26hworf3i"

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attagcactt acacaatcaa cattatgatt gtggcaatct tctgttaatg gatgaagatt 120

aagagaaaaa ttagaacctt gttgtaaaaa ctctgaaaaa gggtccatta aatttactac 180

aaaagaagct tgtaagctgt gatttaatac atcaagtgc aatgtgtgac cagtaacacc 240

atgaaaatct gaaagtacgt gaccattatt tataaacata acatgatatt ccccatgatc 300

<210> 74

<211> 4460

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 74

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aagcgtatta ctagtaaagt gaaacgttat atttctatat taagtacttc tatatatgac 120

gtgtctgttg ttgagttatt taatcggcgt aacaatataa tagatagaat gttgtgctaa 180

aaggatattt tatatttgtg taaaaggatt ttattaatag gggtcctaataacattgggt 240

gaattaaaac atatttttaa taaattcttt atatgtgtag tacatagtga aatagtaaata 300

cttgtgttgt tataaattca tactttttca ctttcaattt aataacgtca ttttctggat 360

aaatagttat gaaactttct ttgtatatag ttagtactat aggtgtgatt atattgttac 420

tttgcttgat gttaattttg tattgtatcg atattgcata tgctaataatt aaaaactgtg 480

ttttcaataa tactgataaa actaaaaatg ctgtgaattt atctattgaa aacaggggta 540

aaaactctgt tttatgtgggt ctaaaaaaag aatttagaag tacattaaga aatttttgtg 600

attataacaa tgtaactct gtagaagcaa aatctgctca atatggtagt ctgatggtaa 660

aagctgggtc taaatacatc caagatttaa tatctgaaat agatgaccga attgttaatc 720

agtatattac tgggagggtta ttatcactag aagtattaat aatgcaattt gaggatacaa 780

tatatactat atgtaatgag gaaactatac agtgcgaact acaaagagtg ctatatgtac 840

gtttgctttt aaataatatt ttaaagttga caaaaagtat atgtgaacaa agtgatattg 900

aattaatgga aatatatgga atgaaatttg aatatgcttt atcttttatt catagtgggt 960

ttacttatat aatgaaaaat atatgtacat taagtggtaa tgtttattgt aataatcaaa 1020  
 aacagttgtg tactgatgat gttactttta ctactatatac attatatgat ataaaccatt 1080  
 gtattagtca ttagataaat ttctaagcct tatttgtatt tgttatgtgg aatgttcaaa 1140  
 tattaggtta attttattca cttagataag tagtgtctat tgggtataaat taacttgtgc 1200  
 tttttattct ataaattgta atagtgtatg tctaatacgt taattcttaa ctatcttggc 1260  
 cagtgttgaa ttattttatt tgctaatttt tactgatgtg aaaagtaaatt attgatatgt 1320  
 aagttatgta atattattta attactaatt tcagttatgt tgcattagta tgacataact 1380  
 gtatatttaa aattatgtat tagtataaatt ttattcaaca gttttgttaa actaagatgt 1440  
 aatttagttt gttgtaagt tagtatttca atttttaatt tttgatatat taatgttagc 1500  
 taggtaatat ataatttgta tatttgatat acaaaatatt agtactattg attatataca 1560  
 tgatcaaatt tggtataatt gtaaggggaaac taaatgagag tttcatttat gtagagaata 1620  
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 aaaaaataaa gttttatata tttaaactag tattaagaa ataaagaatt ataacctgat 1800  
 atgttaagtt atgtgataag gtaacggatt taacaagagc tgtttttttt aacttttatg 1860  
 ttatattaat gtattattta tatgtacata ttatggatca attgggtgat ataaattagg 1920  
 atgatagatc tcaagtatct ttttatattt tgtaattta tattagtttg atcttcatgc 1980  
 taacatcagt actagttatt ttagagaagt agtattaaag tacagggttg tatagtttat 2040  
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 ggaattatta aagagtatta agcttagaat tttcaatttt attgtttatt aagttagtgt 2160  
 aggtactagt ttggtgtcaa tgtattgtag tgaagtaacg tcaggaatta caaatctcca 2220  
 gaatttatct gttgccttac taatgcctat tctgggggtg caaatataat catctatatt 2280  
 gagatttgta ttacaaatgc agaaactatg atttgctgtc atgtctatat tgttatgttc 2340  
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 atttttagat aataagatta tacttcgaat taatattgct gcagggaaac cttcagggtc 2460  
 tgtaacaacg ttgaggcagt gatacattcc atagattaaa taaacataag agaattccagg 2520  
 gttaccaaac attacagcag tgcgctttgt atatccgtgg aaagaatgtg ctgcttgatc 2580

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 catcttgctt agtaagctgc ttgcaacatc aagtgatttt tgtttataaa atgacttctt 2700  
 taatatgttg tacatgtatt gtctttatca ctactatggg actattttaca actaattata 2760  
 ttagtgatgt ataatttttg tcaattaatg gaaatgagct atggatagtg tgaagaaggg 2820  
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 ttcaatatta aagtaagata ctataggtag aattagttag cgtataaaat attaattgcta 3000  
 tagaaggata aattgattaa ggaatatttg tagtatttaa gtaacgtgac tatccatatt 3060  
 tagttatatt ataattgtaa taattatgaa agtattgttt aatgttatct aaattataat 3120  
 gtttttaagt tttcaagtag agttagtaat ttgttggaag catataatat tcataagtta 3180  
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 aattagggta aattgattta ttagcattat aaagattttt ataaattgta caactattcc 3300  
 tacattaatt acctataggg ttattgattt ttcatattat tgtgtgatat actcccatgt 3360  
 gttactgatt aatgggtgtg tatgccgtat agagattttg ctataacttg gttagctata 3420  
 ttgatagcgt gtatcatcac gatattgtga ctaatacatg tgctatgtag gtatgcgttt 3480  
 cctgatctca aaacacgtct agaacgggaa agaaaagcac aggcataaat ggataagtta 3540  
 cttgctaaac aaaacgagtc attagttaat aataaacaag aagaaaagag tgaaaaagag 3600  
 cctgacatat tgtcagaagg tgatactcag ccattaggat gccattgttc aaattcagat 3660  
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 cagctaccac aacttggtgc tagccctact gtatttgaac aagatgagat aagtcaagtt 3780  
 gagtctacaa tggaagggtt acatcctact ggttcaccgt gttgtcgaag acgggctcta 3840  
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 ttttaacagg tgggttattt tagtaaagga gaatcagttg ttgacagttg gagatctatc 3960  
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 ttttagtatct aattaagtag gattgtagat atatggtgtt gttattatac aatattgtta 4080  
 agtctcatga aatgatgct atcaaattgt taatgctatc ataaggctta ttaaatgaaa 4140  
 aatctgtata acgtttttata ttcttttttag ttatgaattt atgtaataata tgtatttgaa 4200  
 tactctaaat tccatttagt taagacaaat tgacttatga gaatgataag tatttagtta 4260

atgattttgc tgtgatatgt attaagtgag tagcgttaga cttgtctttt tcattatttt 4320  
 tgtatataat gtagtgtatt agttaaataa tgggtctgtat tatgcattct gattattaca 4380  
 ctttagctat tataggttca gtaggttttag cactaatcat acttttgtta tgtgttagtc 4440  
 aacttatcaa atatgcgatac 4460

<210> 75  
 <211> 726  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
 <221> CDS  
 <222> (1)..(726)  
 <223> Corresponds to SEQ ID NO:74, nucleotides 369..1094  
 Hypothetical outer membrane protein  
 Product = "27hworf1"

<400> 75  
 atg aaa ctt tct ttg tat ata gtt agt act ata ggt gtg att ata ttg 48  
 Met Lys Leu Ser Leu Tyr Ile Val Ser Thr Ile Gly Val Ile Ile Leu  
 1 5 10 15  
 tta ctt tgc ttg atg tta att ttg tat tgt atc gat att gca tat gct 96  
 Leu Leu Cys Leu Met Leu Ile Leu Tyr Cys Ile Asp Ile Ala Tyr Ala  
 20 25 30  
 aat att aaa aac tgt gtt ttc aat aat act gat aaa act aaa aat gct 144  
 Asn Ile Lys Asn Cys Val Phe Asn Asn Thr Asp Lys Thr Lys Asn Ala  
 35 40 45  
 gtg aat tta tct att gaa aac agg gtt aaa aac tct gtt tta tgt ggt 192  
 Val Asn Leu Ser Ile Glu Asn Arg Val Lys Asn Ser Val Leu Cys Gly  
 50 55 60  
 cta aaa aaa gaa ttt aga agt aca tta aga aat ttt tgt gat tat aac 240  
 Leu Lys Lys Glu Phe Arg Ser Thr Leu Arg Asn Phe Cys Asp Tyr Asn  
 65 70 75 80  
 aat gtt aac tct gta gaa gca aaa tct gct caa tat ggt agt ctg atg 288  
 Asn Val Asn Ser Val Glu Ala Lys Ser Ala Gln Tyr Gly Ser Leu Met  
 85 90 95  
 gta aaa gct ggt tct aaa tac atc caa gat tta ata tct gaa ata gat 336  
 Val Lys Ala Gly Ser Lys Tyr Ile Gln Asp Leu Ile Ser Glu Ile Asp  
 100 105 110  
 gac cga att gtt aat cag tat att act ggg agg gta tta tca cta gaa 384  
 Asp Arg Ile Val Asn Gln Tyr Ile Thr Gly Arg Val Leu Ser Leu Glu  
 115 120 125

gta tta ata atg caa ttt gag gat aca ata tat act ata tgt aat gag 432  
Val Leu Ile Met Gln Phe Glu Asp Thr Ile Tyr Thr Ile Cys Asn Glu  
130 135 140

gaa act ata cag tgc gaa cta caa aga gtg cta tat gta cgt ttg ctt 480  
Glu Thr Ile Gln Cys Glu Leu Gln Arg Val Leu Tyr Val Arg Leu Leu  
145 150 155 160

tta aat aat att tta aag ttg aca aaa agt ata tgt gaa caa agt gat 528  
Leu Asn Asn Ile Leu Lys Leu Thr Lys Ser Ile Cys Glu Gln Ser Asp  
165 170 175

att gaa tta atg gaa ata tat gga atg aaa ttt gaa tat gct tta tct 576  
Ile Glu Leu Met Glu Ile Tyr Gly Met Lys Phe Glu Tyr Ala Leu Ser  
180 185 190

ttt att cat agt ggt ttt act tat ata atg aaa aat ata tgt aca tta 624  
Phe Ile His Ser Gly Phe Thr Tyr Ile Met Lys Asn Ile Cys Thr Leu  
195 200 205

agt ggt aat gtt tat tgt aat aat caa aaa cag ttg tgt act gat gat 672  
Ser Gly Asn Val Tyr Cys Asn Asn Gln Lys Gln Leu Cys Thr Asp Asp  
210 215 220

gtt act ttt act act ata tca tta tat gat ata aac cat tgt att agt 720  
Val Thr Phe Thr Thr Ile Ser Leu Tyr Asp Ile Asn His Cys Ile Ser  
225 230 235 240

cat tag 726  
His

<210> 76  
<211> 241  
<212> PRT  
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 76

Met Lys Leu Ser Leu Tyr Ile Val Ser Thr Ile Gly Val Ile Ile Leu  
1 5 10 15

Leu Leu Cys Leu Met Leu Ile Leu Tyr Cys Ile Asp Ile Ala Tyr Ala  
20 25 30

Asn Ile Lys Asn Cys Val Phe Asn Asn Thr Asp Lys Thr Lys Asn Ala  
35 40 45

Val Asn Leu Ser Ile Glu Asn Arg Val Lys Asn Ser Val Leu Cys Gly  
50 55 60

Leu Lys Lys Glu Phe Arg Ser Thr Leu Arg Asn Phe Cys Asp Tyr Asn  
65 70 75 80

Asn Val Asn Ser Val Glu Ala Lys Ser Ala Gln Tyr Gly Ser Leu Met  
85 90 95

Val Lys Ala Gly Ser Lys Tyr Ile Gln Asp Leu Ile Ser Glu Ile Asp  
100 105 110

Asp Arg Ile Val Asn Gln Tyr Ile Thr Gly Arg Val Leu Ser Leu Glu  
115 120 125

Val Leu Ile Met Gln Phe Glu Asp Thr Ile Tyr Thr Ile Cys Asn Glu  
130 135 140

Glu Thr Ile Gln Cys Glu Leu Gln Arg Val Leu Tyr Val Arg Leu Leu  
145 150 155 160

Leu Asn Asn Ile Leu Lys Leu Thr Lys Ser Ile Cys Glu Gln Ser Asp  
165 170 175

Ile Glu Leu Met Glu Ile Tyr Gly Met Lys Phe Glu Tyr Ala Leu Ser  
180 185 190

Phe Ile His Ser Gly Phe Thr Tyr Ile Met Lys Asn Ile Cys Thr Leu  
195 200 205

Ser Gly Asn Val Tyr Cys Asn Asn Gln Lys Gln Leu Cys Thr Asp Asp  
210 215 220

Val Thr Phe Thr Thr Ile Ser Leu Tyr Asp Ile Asn His Cys Ile Ser  
225 230 235 240

His

<210> 77

<211> 567

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)



<220>  
 <221> misc\_feature  
 <222> (1)..(567)  
 <223> Complement to SEQ ID NO:74, nucleotides 2149..2715  
 Hypothetical DNA-3-methyladenine glycosidase  
 Product = "27hworf2"

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 tacaaatctc cagaatttat ctgttgccct actaatgcct attctggggg tgcaaatata 120  
 atcatctata ttgagatttg tattacaaat gcagaaacta tgatttgctg tcatgtctat 180  
 attgttatgt tcttttggtt tgtgtagggg ttacatatt tttcctgggc cattaacttt 240  
 tgtatgtggt gtatttttag ataataagat tatacttcga attaatttg ctgcagggaa 300  
 accttcaggt tctgtaacaa cgttgaggca gtgatacatt ccatagatta aataaacata 360  
 agagaatcca gggttaccaa acattacagc agtgcgcttt gtatatccgt ggaaagaatg 420  
 tgctgcttga tcatcttgct ctatatatgc ttctgtttct gttataatcc ctttgtgttg 480  
 attaaaaagt aacatcttgc ctagtaagct gcttgcaaca tcaagtgatt tttgtttata 540  
 aaatgacttc tttaatatgt tgtacat 567

<210> 78  
 <211> 240  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
 <221> misc\_feature  
 <222> (1)..(240)  
 <223> Complement to SEQ ID NO:74, nucleotides 3369..3608  
 Product = "27hworf4"

<400> 78  
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 caaaacacgt ctagaacggg aaagaaaagc acaggcaaaa atggataagt tacttgctaa 180  
 acaaaacgag tcattagtta ataataaaca agaagaaaag agtgaaaaag agcctgacat 240

<210> 79  
 <211> 519  
 <212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> CDS

<222> (1)..(519)

<223> Corresponds to SEQ ID NO:74, nucleotides 3382..3900  
Hypothetical lipoprotein  
Product = "27hworf3"

<400> 79

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Met	Pro	Tyr	Arg	Asp	Phe	Ala	Ile	Thr	Trp	Leu	Ala	Ile	Leu	Ile	Ala	
1				5					10					15		

tgt	atc	atc	acg	ata	tgt	gta	cta	ata	cat	gtg	cta	tgt	agg	tat	gcg	96
Cys	Ile	Ile	Thr	Ile	Cys	Val	Leu	Ile	His	Val	Leu	Cys	Arg	Tyr	Ala	
			20					25					30			

ttt	cct	gat	ctc	aaa	aca	cgt	cta	gaa	cgg	gaa	aga	aaa	gca	cag	gca	144
Phe	Pro	Asp	Leu	Lys	Thr	Arg	Leu	Glu	Arg	Glu	Arg	Lys	Ala	Gln	Ala	
		35					40					45				

aaa	atg	gat	aag	tta	ctt	gct	aaa	caa	aac	gag	tca	tta	gtt	aat	aat	192
Lys	Met	Asp	Lys	Leu	Leu	Ala	Lys	Gln	Asn	Glu	Ser	Leu	Val	Asn	Asn	
	50					55				60						

aaa	caa	gaa	gaa	aag	agt	gaa	aaa	gag	cct	gac	ata	ttg	tca	gaa	ggg	240
Lys	Gln	Glu	Glu	Lys	Ser	Glu	Lys	Glu	Pro	Asp	Ile	Leu	Ser	Glu	Gly	
65				70				75						80		

gat	act	cag	cca	tta	gga	tgc	cat	tgt	tca	aat	tca	gat	aaa	ttg	aat	288
Asp	Thr	Gln	Pro	Leu	Gly	Cys	His	Cys	Ser	Asn	Ser	Asp	Lys	Leu	Asn	
			85					90						95		

gat	gag	tct	gta	gag	ttg	cta	gag	gaa	caa	cag	gat	caa	cta	cag	agt	336
Asp	Glu	Ser	Val	Glu	Leu	Leu	Glu	Gln	Gln	Asp	Gln	Leu	Gln	Ser		
			100				105						110			

gaa	cag	cta	cca	caa	ctt	gtg	tct	agc	cct	act	gta	gtt	gaa	caa	gat	384
Glu	Gln	Leu	Pro	Gln	Leu	Val	Ser	Ser	Pro	Thr	Val	Val	Glu	Gln	Asp	
		115				120						125				

gag	ata	agt	caa	gtt	gag	tct	aca	atg	gaa	ggg	tta	cat	cct	act	ggg	432
Glu	Ile	Ser	Gln	Val	Glu	Ser	Thr	Met	Glu	Gly	Leu	His	Pro	Thr	Gly	
	130				135						140					

tca	ccg	tgt	tgt	cga	aga	cgg	gct	cta	act	tct	cta	gtt	agt	gat	gtt	480
Ser	Pro	Cys	Cys	Arg	Arg	Arg	Ala	Leu	Thr	Ser	Leu	Val	Ser	Asp	Val	
145				150					155					160		

atc	att	gag	caa	cag	ggg	aat	agc	caa	ggg	aag	gag	tag				519
Ile	Ile	Glu	Gln	Gln	Gly	Asn	Ser	Gln	Gly	Lys	Glu					
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<210> 80  
 <211> 172  
 <212> PRT  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 80

Met Pro Tyr Arg Asp Phe Ala Ile Thr Trp Leu Ala Ile Leu Ile Ala  
 1 5 10 15

Cys Ile Ile Thr Ile Cys Val Leu Ile His Val Leu Cys Arg Tyr Ala  
 20 25 30

Phe Pro Asp Leu Lys Thr Arg Leu Glu Arg Glu Arg Lys Ala Gln Ala  
 35 40 45

Lys Met Asp Lys Leu Leu Ala Lys Gln Asn Glu Ser Leu Val Asn Asn  
 50 55 60

Lys Gln Glu Glu Lys Ser Glu Lys Glu Pro Asp Ile Leu Ser Glu Gly  
 65 70 75 80

Asp Thr Gln Pro Leu Gly Cys His Cys Ser Asn Ser Asp Lys Leu Asn  
 85 90 95

Asp Glu Ser Val Glu Leu Leu Glu Glu Gln Gln Asp Gln Leu Gln Ser  
 100 105 110

Glu Gln Leu Pro Gln Leu Val Ser Ser Pro Thr Val Val Glu Gln Asp  
 115 120 125

Glu Ile Ser Gln Val Glu Ser Thr Met Glu Gly Leu His Pro Thr Gly  
 130 135 140

Ser Pro Cys Cys Arg Arg Arg Ala Leu Thr Ser Leu Val Ser Asp Val  
 145 150 155 160

Ile Ile Glu Gln Gln Gly Asn Ser Gln Gly Lys Glu  
 165 170

<210> 81  
 <211> 560  
 <212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> misc\_feature

<222> (560)..(560)

<223> n = a, c, g, or t

<400> 81

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tcaacttaac aacacagatt tattattata aacactatta aaaaaataac aagatacaca      180
ctatgaatca gataaccttg gtattctaata atacgtatga tataatgata ctaaaccata      240
agtttatatt atttaaagac ataatgacat atctttaaat gctaatatgt ataattcttaa      300
agtccttaag atacatacat ttatagacat atctgtaata atgcactata taatgttaag      360
atgtatagtc aataagtttg tgtttaatga gaatagaatg caaaaattgc aaagcagttt      420
atagaataga caatagcaaa attccatta atggtaaaaa agttaagtt aaatgcacaa      480
actgtaatac tacatggatg cacataccaa ctcaagataa agcaatacct gaagaagaaa      540
aacaattagt aataggatcn      560

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<210> 82

<211> 174

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>

<221> CDS

<222> (1)..(174)

<223> Corresponds to SEQ ID NO:81, nucleotides 387..>559  
Product = "lgdorfli"

<220>

<221> misc\_feature

<222> (174)..(174)

<223> n = a, c, g, or t.

<220>

<221> misc\_feature

<222> (172)..(174)

<223> Xaa = Ser

<400> 82

atg aga ata gaa tgc aaa aat tgc aaa gca gtt tat aga ata gac aat 48  
Met Arg Ile Glu Cys Lys Asn Cys Lys Ala Val Tyr Arg Ile Asp Asn  
1 5 10 15

agc aaa att ccc att aat ggt aaa aaa gtt aaa gtt aaa tgc aca aac 96  
Ser Lys Ile Pro Ile Asn Gly Lys Lys Val Lys Val Lys Cys Thr Asn  
20 25 30

tgt aat act aca tgg atg cac ata cca act caa gat aaa gca ata cct 144  
Cys Asn Thr Thr Trp Met His Ile Pro Thr Gln Asp Lys Ala Ile Pro  
35 40 45

gaa gaa gaa aaa caa tta gta ata gga tcn 174  
Glu Glu Glu Lys Gln Leu Val Ile Gly Xaa  
50 55

<210> 83  
<211> 58  
<212> PRT  
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
<221> misc\_feature  
<222> (58)..(58)  
<223> The 'Xaa' at location 58 stands for Ser.

<220>  
<221> misc\_feature  
<222> (174)..(174)  
<223> n = a, c, g, or t.

<220>  
<221> misc\_feature  
<222> (172)..(174)  
<223> Xaa = Ser

<400> 83

Met Arg Ile Glu Cys Lys Asn Cys Lys Ala Val Tyr Arg Ile Asp Asn  
1 5 10 15

Ser Lys Ile Pro Ile Asn Gly Lys Lys Val Lys Val Lys Cys Thr Asn  
20 25 30

Cys Asn Thr Thr Trp Met His Ile Pro Thr Gln Asp Lys Ala Ile Pro  
35 40 45

Glu Glu Glu Lys Gln Leu Val Ile Gly Xaa  
50 55

<210> 84  
 <211> 2008  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 84  
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 actgtgaaca aatttcgttg tggagatact gtaagtataa agtacgatat acgtgaacta 180  
 aacggtaata cgatactaca agatcaagaa ttaaaattta ctattggaaa aaatgaagtc 240  
 cctcttgcaa tagagctagg tgtaattaat atgagacaag acatggcaag acatattatt 300  
 gcaccattag aacttttgac taattttgac aaacctgaca acttttgatg aatacaaaat 360  
 aaaactaatt gatattacct acattaatca accacaacct atacaaaaaa acgcaaagcc 420  
 cageccaatct taagggtgatt atttcttata tctgtatagc cacataaaaa agctaaaaat 480  
 aacggttatta tatcaaataa attacaatca acaatactac actaatatta tagaaatcta 540  
 ctaatatatt gatatagtaa aataatacac atttacacaa tcaatactta aattcataat 600  
 aacttggtgc aactttataa aaccagctat ttcataaaaa taacacaaaa ctataaaaca 660  
 ccaaatagct tactcacgct aaatgtttct ataaataaat caacttgta ttgtaataat 720  
 ataaaaactc accaatttta ataaaacaaa tatatactaa tcttttattt cctaatttat 780  
 cttaataaga ttcaatatcc ttatacta ataaatctta actcatatat taccacccca 840  
 cactaacaaa tccatagaac ttgctaagtg tatattatat aatattaatt taacatgta 900  
 atgactgaaa aagtattaac ttaaagatct atttaataaa atttaacctc ttctataacc 960  
 ttaactatca tcatttttaa gtaactgaag tatttaagac atttaacaat tatatatcat 1020  
 ataaaaatct ttaatgtact agcaattgat gaattatgcc ctcataatat atgcaagcat 1080  
 aaaatgccta ttttaacaaa actttatcta ttctataacc ttaactatta ccatttttaa 1140  
 gtaactgagg tatttaagac atttaataat tatataccat ataaaaatct gcttaatgta 1200  
 ctagcaattg atgaattatt ccctcataat atatgcaagc ataaaatgcc taatttaaca 1260  
 aaactttatc tattctataa ccttaactat tactattttc aagtaactga agtatttaag 1320  
 atatttgaca attatatatc atattaaaat ctgcttaatg tactagcaat tgatggatta 1380  
 ttctctcata atatatgtaa gcataaaatg cctaatttaa taaaacttta tctattctat 1440  
 aacttaacta ttactatttt caagtaactg aagtatttaa gatatttgac aattatatat 1500

catatcaaaa tctgcttaat gtactagcaa ttgatggatt attctctcat aatatatgta 1560  
 agcataaaat gcctaattta ataaaacttt atctattcta taaccttaac tattactatt 1620  
 ttcaagtaac tgaagtattt aagatatttg acaattatat atcatataaa aatctttaat 1680  
 gtactagcaa ttgacaacta tgccttgata atctatgtag cataaaatac ctcatttaac 1740  
 aaaactttat ctattctata accttaacta ttaccatttt taagtaactg aagtatttaa 1800  
 gatatttgac aattatatat catataaaaa tctttaatgt actagcaatt gacaactatt 1860  
 ccctgataat ctatgtagca taaaatacct acaggaatct ttattaatag taatttactt 1920  
 atctattgaa cataacttta agtattacta gtcataatat tataaagaca catttaatat 1980  
 taaacattgt agacatttta acatgatc 2008

<210> 85  
 <211> 348  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
 <221> CDS  
 <222> (1)..(348)  
 <223> Corresponds to SEQ ID NO:84, nucleotides <1..348  
 Product = "2gdorfli"

<400> 85  
 gat caa aaa ggg ata cca aaa gag caa tac tat ata aaa tta gta tct 48  
 Asp Gln Lys Gly Ile Pro Lys Glu Gln Tyr Tyr Ile Lys Leu Val Ser  
 1 5 10 15  
 gtt aat tca aca tat cct gac tca att aat aac tta ctc ata ttt agt 96  
 Val Asn Ser Thr Tyr Pro Asp Ser Ile Asn Asn Leu Leu Ile Phe Ser  
 20 25 30  
 agt att att gaa agc tat gaa ggc act gtg aac aaa ttt cgt tgt gga 144  
 Ser Ile Ile Glu Ser Tyr Glu Gly Thr Val Asn Lys Phe Arg Cys Gly  
 35 40 45  
 gat act gta agt ata aag tac gat ata cgt gaa cta aac ggt aat acg 192  
 Asp Thr Val Ser Ile Lys Tyr Asp Ile Arg Glu Leu Asn Gly Asn Thr  
 50 55 60  
 ata cta caa gat caa gaa tta aaa ttt act att gga aaa aat gaa gtc 240  
 Ile Leu Gln Asp Gln Glu Leu Lys Phe Thr Ile Gly Lys Asn Glu Val  
 65 70 75 80  
 cct ctt gca ata gag cta ggt gta att aat atg aga caa gac atg gca 288  
 Pro Leu Ala Ile Glu Leu Gly Val Ile Asn Met Arg Gln Asp Met Ala

85

90

95

aga cat att att gca cca tta gaa ctt ttg act aat ttt gac aaa cct 336  
 Arg His Ile Ile Ala Pro Leu Glu Leu Leu Thr Asn Phe Asp Lys Pro  
           100                  105                  110

gac aac ttt tga 348  
 Asp Asn Phe  
           115

&lt;210&gt; 86

&lt;211&gt; 115

&lt;212&gt; PRT

&lt;213&gt; Ehrlichia ruminantium (formerly Cowdria ruminantium)

&lt;400&gt; 86

Asp Gln Lys Gly Ile Pro Lys Glu Gln Tyr Tyr Ile Lys Leu Val Ser  
 1                  5                  10                  15

Val Asn Ser Thr Tyr Pro Asp Ser Ile Asn Asn Leu Leu Ile Phe Ser  
           20                  25                  30

Ser Ile Ile Glu Ser Tyr Glu Gly Thr Val Asn Lys Phe Arg Cys Gly  
           35                  40                  45

Asp Thr Val Ser Ile Lys Tyr Asp Ile Arg Glu Leu Asn Gly Asn Thr  
           50                  55                  60

Ile Leu Gln Asp Gln Glu Leu Lys Phe Thr Ile Gly Lys Asn Glu Val  
           65                  70                  75                  80

Pro Leu Ala Ile Glu Leu Gly Val Ile Asn Met Arg Gln Asp Met Ala  
                   85                  90                  95

Arg His Ile Ile Ala Pro Leu Glu Leu Leu Thr Asn Phe Asp Lys Pro  
           100                  105                  110

Asp Asn Phe  
           115

&lt;210&gt; 87

&lt;211&gt; 3829

&lt;212&gt; DNA

&lt;213&gt; Ehrlichia ruminantium (formerly Cowdria ruminantium)



<400> 87  
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gacaaattaa tcaatacctt aaaatgagtt gagtggaaaa gtataaataa tgtaggtggt 120  
ttttttgttt ataattgaat taaagtgctt aaagatattt atatagttat tacttagatt 180  
atttaattaa attaagctag tgaacaaaga atttgtatta tatatatattt aggtatctat 240  
tatctttaca gtttaaataa gaaagcaagg gtttattaat tatatagtga atgaaatata 300  
ttattactga gtatatcatg tttattatat acattattca ctattcacia attcagtga 360  
tgtgataaac ctaaataatt atacaaatat tagggggggg gggggtatat ttttcgtaa 420  
gagcttacat taatgtaatt attaatagta tttttgttt ttaaaagatg taaattctac 480  
tgttgtttgt tactgcataa caatattcag tgataaacia ggatttacia taaatacact 540  
tgccttttta agaataattt agtagtttg agaatcatat gatacttgat gatgagtata 600  
cctaagagt agttcgttac ctgttttaca gggtattata cttttacttt ctgcagtaat 660  
atgtgcttta ttaaaaaata gtacattggg gaaaattata tcatctattg ttgtagtagt 720  
atctttttcc attgcgttgg tattgttctc tcaggtttat tctgctgatg taatcaaata 780  
cagcctaggg ggggtgggtcg ttccttatgg catagaactt aaagtgaaca tatttagtgc 840  
tactatgctt gtttttagtaa attttattgc tgtaatgagt atattgtatg gcatatatcc 900  
taacatcaga gaaataggtg ttaacaagat accaagtttc tattctgtat ttttgctatg 960  
tttaggtggc tttttgggga tattagtatc aaatgatgtt tttaatatct atgtttttct 1020  
tgagatttcg tctatttctt cttatatattt gggtgcaatg ggaaaagata aagctgcttt 1080  
aatagcagca tttgattatt tagtaattgg tacaattggg gcaacttttt atttaatagg 1140  
tataggcttt ttgtatgcta ttaactggta attgaatatt ggagatttgt ttctaataat 1200  
tcatgataat ttgctggtaa caaatagagt tacacagatt gcaatgttat ttattatggg 1260  
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attgccattt	attatattat	gtttaagttt	aattggatatg	ccagttactt	cagggtttat	1800
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gttgcttata	ggttctgggt	tatctatagt	gtatgtttgg	aaaatagttg	aagcagtgtg	1920
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attatgtatt	tggataatgg	taattgcttc	gattattgtg	ggaatatatc	caattccttt	2040
aacattgatt	tctaataaaa	tagcgacgtt	gctattatat	tgagatatct	atTTgaattt	2100
tattattact	aatgggttta	tttagatggg	gagttacact	caagtaataa	taaaaaatgt	2160
caattaacta	cccattccta	ggtaattttat	acctaactat	taactaatca	ttcttatgag	2220
gaaaatgtag	taaacattac	taccttacat	aataactatg	taaaaatcta	aagaaatacc	2280
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agtataattc	ctatcaaagt	gtttatccat	actacctata	ttttcttgag	tacttacaga	2460
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actacctatc	actaatagaa	gtattagtaa	cgctattgac	tttgggttac	taactatata	2580
taataataag	ttataaaaaat	catttagcat	aacattatct	taaataacca	taacacaact	2640
atcattatat	tccaaaaatg	catataagca	tagtaaataa	ttaatgctat	agcatgtttt	2700
ttgttttgcc	tgtaaagtta	agttgtaatc	attaaataag	tttattttca	ctttgtaata	2760
tattactgta	tttgcttagt	tttcgtataa	ttctaccact	tacttcaatc	agccttatat	2820
ttactggtaa	taatgcaatt	cttccttaat	attaatagtt	aatataaata	aattaatact	2880
taattataac	ataagtttaa	gaatattact	agtaatgtat	tgctgttggt	tgatttttat	2940
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ataattgagc	ttttattgat	ggtaattact	taaattttat	gtaaactcaa	taatgtcaaa	3120
tatttatatt	atctttatct	agttgttcat	cctattagtt	agttataata	tgcttggtgt	3180
caaatttgta	tttaacaatt	gatattgact	acttaataag	tgaatctatt	atTTtagcaa	3240
taattgcatt	gaaacttaaa	tctgaatgtg	tatgttctat	taaaccttca	cttacgatga	3300

cttcttgatc tgatccaagt tcgatatcaa tgtgcttttt tcctaacata ttgctgttta 3360  
 atatagatgc tgaactatct gaaggtagta agatattttt ctgtatgcac attggttacta 3420  
 taggagtata gctttcattc aatgatattg aagttactgt acctattttt actcctgata 3480  
 ttgttacttc atctcctatg tccaacccat ctacatttga gaaaaatgct ttaactgtat 3540  
 aacaattacg caaggatattt ttatatggta atttggttaa tgctattatc ccaatagata 3600  
 ttgctcctgc taacactagg aatcctataa aaatttcaat aatatttgat ctatgcataa 3660  
 aataccgatg ttaatatggt ttgtgttatt taaaagactt ttgaggatgg taggcgtact 3720  
 tagttccggt taaatttggt acatgtagat ttttttctgc aagtgttggg aattgattat 3780  
 ctgtataatg taaccatata tgccataatg caggaacttt tgttggatc 3829

<210> 88  
 <211> 1479  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)  
 <220>  
 <221> CDS  
 <222> (1)..(1479)  
 <223> Corresponds to SEQ ID NO:87, nucleotides 605..2083  
 Hypothetical NADH dehydrogenase (ubiquinone)  
 Product = "3gdorf1"

<400> 88  
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 1 5 10 15  
 gca gta ata tgt gct tta tta aaa aat agt aca ttg gtg aaa att ata 96  
 Ala Val Ile Cys Ala Leu Leu Lys Asn Ser Thr Leu Val Lys Ile Ile  
 20 25 30  
 tca tct att gtt gta gta gta tct ttt tcc att gcg ttg gta ttg ttc 144  
 Ser Ser Ile Val Val Val Val Ser Phe Ser Ile Ala Leu Val Leu Phe  
 35 40 45  
 tct cag gtt tat tct gct gat gta atc aaa tac agc cta ggg ggg tgg 192  
 Ser Gln Val Tyr Ser Ala Asp Val Ile Lys Tyr Ser Leu Gly Gly Trp  
 50 55 60  
 gtc gtt cct tat ggc ata gaa ctt aaa gtg aac ata ttt agt gct act 240  
 Val Val Pro Tyr Gly Ile Glu Leu Lys Val Asn Ile Phe Ser Ala Thr  
 65 70 75 80  
 atg ctt gtt tta gta aat ttt att gct gta atg agt ata ttg tat ggc 288

Met	Leu	Val	Leu	Val	Asn	Phe	Ile	Ala	Val	Met	Ser	Ile	Leu	Tyr	Gly		
				85					90					95			
ata	tat	cct	aac	atc	aga	gaa	ata	ggg	gtt	aac	aag	ata	cca	agt	ttc	336	
Ile	Tyr	Pro	Asn	Ile	Arg	Glu	Ile	Gly	Val	Asn	Lys	Ile	Pro	Ser	Phe		
			100					105					110				
tat	tct	gta	ttt	ttg	cta	tgt	tta	ggg	ggc	ttt	ttg	ggg	ata	tta	gta	384	
Tyr	Ser	Val	Phe	Leu	Leu	Cys	Leu	Gly	Gly	Phe	Leu	Gly	Ile	Leu	Val		
			115				120					125					
tca	aat	gat	gtt	ttt	aat	atc	tat	gtt	ttt	ctt	gag	att	tcg	tct	att	432	
Ser	Asn	Asp	Val	Phe	Asn	Ile	Tyr	Val	Phe	Leu	Glu	Ile	Ser	Ser	Ile		
		130				135					140						
tct	tct	tat	att	ttg	gtt	gca	atg	gga	aaa	gat	aaa	gct	gct	tta	ata	480	
Ser	Ser	Tyr	Ile	Leu	Val	Ala	Met	Gly	Lys	Asp	Lys	Ala	Ala	Leu	Ile		
					150					155					160		
gca	gca	ttt	gat	tat	tta	gta	att	ggg	aca	att	ggg	gca	act	ttt	tat	528	
Ala	Ala	Phe	Asp	Tyr	Leu	Val	Ile	Gly	Thr	Ile	Gly	Ala	Thr	Phe	Tyr		
				165					170					175			
tta	ata	ggg	ata	ggc	ttt	ttg	tat	gct	att	act	ggg	aca	ttg	aat	att	576	
Leu	Ile	Gly	Ile	Gly	Phe	Leu	Tyr	Ala	Ile	Thr	Gly	Thr	Leu	Asn	Ile		
				180				185					190				
gga	gat	ttg	ttt	cta	ata	att	cat	gat	aat	ttg	ctg	gta	aca	aat	aga	624	
Gly	Asp	Leu	Phe	Leu	Ile	Ile	His	Asp	Asn	Leu	Leu	Val	Thr	Asn	Arg		
			195				200					205					
gtt	aca	cag	att	gca	atg	tta	ttt	att	atg	gta	ggg	ttg	ttt	ata	aag	672	
Val	Thr	Gln	Ile	Ala	Met	Leu	Phe	Ile	Met	Val	Gly	Leu	Phe	Ile	Lys		
			210			215					220						
aca	gcg	cta	ttc	cca	ttt	cat	aaa	tgg	tta	ata	cag	gct	tat	agt	ttt	720	
Thr	Ala	Leu	Phe	Pro	Phe	His	Lys	Trp	Leu	Ile	Gln	Ala	Tyr	Ser	Phe		
					230					235					240		
gct	cct	tct	ttt	att	tct	gtg	ttt	ttt	tcc	ggg	act	tct	act	aaa	gtt	768	
Ala	Pro	Ser	Phe	Ile	Ser	Val	Phe	Phe	Ser	Gly	Thr	Ser	Thr	Lys	Val		
				245					250					255			
atg	ata	tat	cta	att	ata	aag	atg	ata	tat	gac	gtt	ttt	aaa	gct	gat	816	
Met	Ile	Tyr	Leu	Ile	Ile	Lys	Met	Ile	Tyr	Asp	Val	Phe	Lys	Ala	Asp		
			260					265					270				
ttt	gtt	ttt	gtg	act	tta	cct	ttt	aat	att	gtt	ttt	atg	tgt	ttt	gct	864	
Phe	Val	Phe	Val	Thr	Leu	Pro	Phe	Asn	Ile	Val	Phe	Met	Cys	Phe	Ala		
			275				280					285					
gtg	ttg	tca	ata	gtt	tgt	gga	tct	tta	ctt	gca	att	ttt	act	agc	aat	912	
Val	Leu	Ser	Ile	Val	Cys	Gly	Ser	Leu	Leu	Ala	Ile	Phe	Thr	Ser	Asn		
			290			295					300						

att aaa aag ata ttt gct tat tca agt att gca cat tta gga tat att 960  
 Ile Lys Lys Ile Phe Ala Tyr Ser Ser Ile Ala His Leu Gly Tyr Ile  
 305 310 315 320

gta ttt gca gtt agt tta aat act aat tat ggt ttg gtt gca gct ata 1008  
 Val Phe Ala Val Ser Leu Asn Thr Asn Tyr Gly Leu Val Ala Ala Ile  
 325 330 335

gct tat att att agt cat agc ttg gtt aag tca gca tta ttt atg att 1056  
 Ala Tyr Ile Ile Ser His Ser Leu Val Lys Ser Ala Leu Phe Met Ile  
 340 345 350

gta ggt agc att gat tat agt tgt ggt aac aga cat ctg aaa gat tgt 1104  
 Val Gly Ser Ile Asp Tyr Ser Cys Gly Asn Arg His Leu Lys Asp Cys  
 355 360 365

gca aac atg tgg gaa acc atg cca aaa att aca ttg cca ttt att ata 1152  
 Ala Asn Met Trp Glu Thr Met Pro Lys Ile Thr Leu Pro Phe Ile Ile  
 370 375 380

tta tgt tta agt tta att ggt atg cca gtt act tca ggg ttt att gct 1200  
 Leu Cys Leu Ser Leu Ile Gly Met Pro Val Thr Ser Gly Phe Ile Ala  
 385 390 395 400

aaa tgg tat att gtt gat gca gtt ata aag tct aat ttt tgg gtt ggt 1248  
 Lys Trp Tyr Ile Val Asp Ala Val Ile Lys Ser Asn Phe Trp Val Gly  
 405 410 415

att ttt gtg ttg ctt ata ggt tct ggg tta tct ata gtg tat gtt tgg 1296  
 Ile Phe Val Leu Leu Ile Gly Ser Gly Leu Ser Ile Val Tyr Val Trp  
 420 425 430

aaa ata gtt gaa gca gtg tgt ctt cgt tca cct gat aat aag gta gtt 1344  
 Lys Ile Val Glu Ala Val Cys Leu Arg Ser Pro Asp Asn Lys Val Val  
 435 440 445

atg tcg tcg ttt gaa aca cca aat gtt atg gta tta tgt att tgg ata 1392  
 Met Ser Ser Phe Glu Thr Pro Asn Val Met Val Leu Cys Ile Trp Ile  
 450 455 460

atg gta att gct tcg att att gtg gga ata tat cca att cct tta aca 1440  
 Met Val Ile Ala Ser Ile Ile Val Gly Ile Tyr Pro Ile Pro Leu Thr  
 465 470 475 480

ttg att tct aat aaa ata gcg acg ttg cta tta tat tga 1479  
 Leu Ile Ser Asn Lys Ile Ala Thr Leu Leu Leu Tyr  
 485 490

&lt;210&gt; 89

&lt;211&gt; 492

&lt;212&gt; PRT

&lt;213&gt; Ehrlichia ruminantium (formerly Cowdria ruminantium)

&lt;400&gt; 89

Met Ser Ser Ser Leu Pro Val Leu Gln Val Ile Ile Pro Leu Leu Ser  
1 5 10 15

Ala Val Ile Cys Ala Leu Leu Lys Asn Ser Thr Leu Val Lys Ile Ile  
20 25 30

Ser Ser Ile Val Val Val Val Ser Phe Ser Ile Ala Leu Val Leu Phe  
35 40 45

Ser Gln Val Tyr Ser Ala Asp Val Ile Lys Tyr Ser Leu Gly Gly Trp  
50 55 60

Val Val Pro Tyr Gly Ile Glu Leu Lys Val Asn Ile Phe Ser Ala Thr  
65 70 75 80

Met Leu Val Leu Val Asn Phe Ile Ala Val Met Ser Ile Leu Tyr Gly  
85 90 95

Ile Tyr Pro Asn Ile Arg Glu Ile Gly Val Asn Lys Ile Pro Ser Phe  
100 105 110

Tyr Ser Val Phe Leu Leu Cys Leu Gly Gly Phe Leu Gly Ile Leu Val  
115 120 125

Ser Asn Asp Val Phe Asn Ile Tyr Val Phe Leu Glu Ile Ser Ser Ile  
130 135 140

Ser Ser Tyr Ile Leu Val Ala Met Gly Lys Asp Lys Ala Ala Leu Ile  
145 150 155 160

Ala Ala Phe Asp Tyr Leu Val Ile Gly Thr Ile Gly Ala Thr Phe Tyr  
165 170 175

Leu Ile Gly Ile Gly Phe Leu Tyr Ala Ile Thr Gly Thr Leu Asn Ile  
180 185 190

Gly Asp Leu Phe Leu Ile Ile His Asp Asn Leu Leu Val Thr Asn Arg  
195 200 205

Val Thr Gln Ile Ala Met Leu Phe Ile Met Val Gly Leu Phe Ile Lys  
210 215 220

Thr Ala Leu Phe Pro Phe His Lys Trp Leu Ile Gln Ala Tyr Ser Phe  
225 230 235 240

Ala Pro Ser Phe Ile Ser Val Phe Phe Ser Gly Thr Ser Thr Lys Val  
245 250 255

Met Ile Tyr Leu Ile Ile Lys Met Ile Tyr Asp Val Phe Lys Ala Asp  
260 265 270

Phe Val Phe Val Thr Leu Pro Phe Asn Ile Val Phe Met Cys Phe Ala  
275 280 285

Val Leu Ser Ile Val Cys Gly Ser Leu Leu Ala Ile Phe Thr Ser Asn  
290 295 300

Ile Lys Lys Ile Phe Ala Tyr Ser Ser Ile Ala His Leu Gly Tyr Ile  
305 310 315 320

Val Phe Ala Val Ser Leu Asn Thr Asn Tyr Gly Leu Val Ala Ala Ile  
325 330 335

Ala Tyr Ile Ile Ser His Ser Leu Val Lys Ser Ala Leu Phe Met Ile  
340 345 350

Val Gly Ser Ile Asp Tyr Ser Cys Gly Asn Arg His Leu Lys Asp Cys  
355 360 365

Ala Asn Met Trp Glu Thr Met Pro Lys Ile Thr Leu Pro Phe Ile Ile  
370 375 380

Leu Cys Leu Ser Leu Ile Gly Met Pro Val Thr Ser Gly Phe Ile Ala  
385 390 395 400

Lys Trp Tyr Ile Val Asp Ala Val Ile Lys Ser Asn Phe Trp Val Gly  
405 410 415

Ile Phe Val Leu Leu Ile Gly Ser Gly Leu Ser Ile Val Tyr Val Trp  
420 425 430

Lys Ile Val Glu Ala Val Cys Leu Arg Ser Pro Asp Asn Lys Val Val

435

440

445

Met Ser Ser Phe Glu Thr Pro Asn Val Met Val Leu Cys Ile Trp Ile  
 450 455 460

Met Val Ile Ala Ser Ile Ile Val Gly Ile Tyr Pro Ile Pro Leu Thr  
 465 470 475 480

Leu Ile Ser Asn Lys Ile Ala Thr Leu Leu Leu Tyr  
 485 490

<210> 90  
 <211> 300  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
 <221> misc\_feature  
 <222> (1)..(300)  
 <223> Complement to SEQ ID NO:87, nucleotides 2311..2610  
 Product = "3gdorf2"

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 actacctata ttttcttgag tacttacaga tgattgatct ttaggttgaa gctttttctt 180  
 aagtttttta ttgtacttaa agaaataagt actacctatc actaatagaa gtattagtaa 240  
 cgctattgac tttgggttac taactatata taataataag ttataaaaat catttagcat 300

<210> 91  
 <211> 450  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
 <221> misc\_feature  
 <222> (1)..(450)  
 <223> Complement to SEQ ID NO:87, nucleotides 3209..3658  
 Hypothetical outer membrane protein, related to proposed ABC tran  
 sporter  
 Product = "3gdorf3"

<400> 91  
 ctacttaata agtgaatcta ttatttttagc aataattgca ttgaaactta aatctgaatg 60



tgtatgttct attaaacctt cacttacgat gactttctga tctgatccaa gttcgatatc 120  
aatgtgcttt tttcctaaca tattgctggt taatatagat gctgaactat ctgaaggtag 180  
taagatattt ttctgtatgc acattgttac tataggagta tagctttcat tcaatgatat 240  
tgaagttact gtacctattt ttactcctga tattgttact tcatctccta tgtccaaccc 300  
atctacattt gagaaaaatg ctttaactgt ataacaatta cgcaagggtat ttttatatgg 360  
taatttgtaa aatgctatta tccaataga tattgctcct gctaacta ggaatcctat 420  
aaaaatttca ataattttg atctatgcat 450

<210> 92  
<211> 226  
<212> DNA  
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 92  
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ctataatagt agcaccttta ataggagatg taactttccc atcttctatt aagtagcttt 120  
cagaagctga aaaaacaaat ttaccagatg taatatctac ctgaccacca gcaaaattca 180  
cagcataaat tcctttcttc acactagcaa tgatttcatt tggatc 226

<210> 93  
<211> 226  
<212> DNA  
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
<221> misc\_feature  
<222> (1)..(226)  
<223> Complement to SEQ ID NO:92, nucleotides <1..>226  
Hypothetical tldD protein  
Product = "4gdorf1i"

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ctataatagt agcaccttta ataggagatg taactttccc atcttctatt aagtagcttt 120  
cagaagctga aaaaacaaat ttaccagatg taatatctac ctgaccacca gcaaaattca 180  
cagcataaat tcctttcttc acactagcaa tgatttcatt tggatc 226

<210> 94

<211> 160  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 94  
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 gagcagcccg gcgtggccga gctggggcgac gccgtcgggc gtcgacagcg tgcccatatg 120  
 cgccgtgatc ggcaggccgt gggcgcgggc gaactcgatc 160

<210> 95  
 <211> 299  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 95  
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 gcttttagtt acagaaaatt tcattaaaca taacaatgga atacaaaaaattagagagct 120  
 tagtaaacia aaaaatattt acccaaaaaca agtaaataatc aatactatca actcagtact 180  
 accacctaata agtaaccacc aaggcattgc tttaacaagtt tcaatagtag atacagtaag 240  
 catagaagac gtattatcta atattcctac agagatttca acaataatac ttttagatc 299

<210> 96  
 <211> 297  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
 <221> CDS  
 <222> (1)..(297)  
 <223> Corresponds to SEQ ID NO:95, nucleotides <1..>297  
 Product = "6gdorfli"

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 Ile Tyr Gly Lys His Pro Cys Val Ala Ala Leu Gln Asn Ile Asn Arg  
 1 5 10 15  
 aaa tgt cat gag ctt tta gtt aca gaa aat ttc att aaa cat aac aat 96  
 Lys Cys His Glu Leu Leu Val Thr Glu Asn Phe Ile Lys His Asn Asn  
 20 25 30  
 gga ata caa aaa att aga gag ctt agt aaa caa aaa aat att tac cca 144  
 Gly Ile Gln Lys Ile Arg Glu Leu Ser Lys Gln Lys Asn Ile Tyr Pro  
 35 40 45  
 aaa caa gta aat atc aat act atc aac tca gta cta cca cct aat agt 192

Lys Gln Val Asn Ile Asn Thr Ile Asn Ser Val Leu Pro Pro Asn Ser  
 50 55 60  
 aac cac caa ggc att gct tta caa gtt tca ata gta gat aca gta agc 240  
 Asn His Gln Gly Ile Ala Leu Gln Val Ser Ile Val Asp Thr Val Ser  
 65 70 75 80  
 ata gaa gac gta tta tct aat att cct aca gag att tca aca ata ata 288  
 Ile Glu Asp Val Leu Ser Asn Ile Pro Thr Glu Ile Ser Thr Ile Ile  
 85 90 95  
 ctt tta gat 297  
 Leu Leu Asp

<210> 97  
 <211> 99  
 <212> PRT  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 97

Ile Tyr Gly Lys His Pro Cys Val Ala Ala Leu Gln Asn Ile Asn Arg  
 1 5 10 15

Lys Cys His Glu Leu Leu Val Thr Glu Asn Phe Ile Lys His Asn Asn  
 20 25 30

Gly Ile Gln Lys Ile Arg Glu Leu Ser Lys Gln Lys Asn Ile Tyr Pro  
 35 40 45

Lys Gln Val Asn Ile Asn Thr Ile Asn Ser Val Leu Pro Pro Asn Ser  
 50 55 60

Asn His Gln Gly Ile Ala Leu Gln Val Ser Ile Val Asp Thr Val Ser  
 65 70 75 80

Ile Glu Asp Val Leu Ser Asn Ile Pro Thr Glu Ile Ser Thr Ile Ile  
 85 90 95

Leu Leu Asp

<210> 98  
 <211> 2104  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 98  
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cattttacca gaatgatgaa taatgacatt tcataaagtt taataaataa ggatttataa 180  
tgaatgctaa agaaaaaat attagagaag aaatttttaa tcttcaaaaa aagattgctg 240  
aatgagacaa tgcttattat aatttggata atcctattgt aactgatgaa atttatgata 300  
ctgagtttat tagacttcaa aaattagaaa aacaatatag tcatttgcta acttatgaag 360  
aagttaaaaa ctctccaacg caaaaaattg atgcaaagtc tttatcaata tttgataaag 420  
taattcataa aaaaccaatg ctttctttaa acaaagcata ttcaattgaa gaaattaaga 480  
aattttattaa aaagattgaa aaatatacta atgatttttc attttttatt gaacctaaaa 540  
ttgatggtct ttctatttca ttaacttatg aaaatggaaa actaattaga ggtgtaacta 600  
gaggagatgg aataacagga gaagatgtta caaaaaatat tttacaaatt aatgatatcc 660  
ctaaagaaat agaatacaaa cacaaaatcg aattaagagg aaaaatatat ttatctattt 720  
ctagatttaa tgaattaaat gaagaaaatt taaaaataa tttaccgcct ttagctaacc 780  
caagaaatgc agcagccgga actttaagac aattagattc taatattggt tctcaaagag 840  
ggttgtcatc ttttatatat tttgtagtcg atgctcccag tcataatatt tggacaatgg 900  
aagatgcctt ttgttttctt aagaaaaata attttcatgt tgtaaaagat tataaactag 960  
ctaaaaatat taatcaaatt gaagaatata taaataattt tccagaactt aaaaaaacat 1020  
ttgattttga agcagatggg gtagttatta aattaaatga aattaaatga tgaaataaaa 1080  
ttggacaaac tcaaaaagtt ccacattatg cgattgcttt taaatttgaa ccaaacattg 1140  
aaattacaac aattaaaaag atatttataa ctattggaag aactggccta gtcacttata 1200  
atggccaagt taaaactgtc gaaatttctg gttccaaaat aaactttgca acattaaata 1260  
attttaatta cgttaaagaa ctaaatttaa atgttggcga tgaagtttat attaaaaagg 1320  
ctggtgaaat tattccttgc attataggac tagttaatcc aaaaggtaaa cctgattatt 1380  
ttaaagaat agaaacttgc ccatattgta attctaaatt aatagaaagt gaaacattct 1440  
tagaagaata ttgtgaaaat tacaattgtc cagaaattat aaaaaacaa ctaattcatt 1500  
tttcttcaaa agaatgtatg aatttctttt caatgggcga aaaaatagta gaaaaattat 1560  
atgaaaataa attaatctt agtccactag atttttataa tttaaaaaat aataaaaatg 1620

aactaacaca attagaaaaa ttaggaacta aatctataat gaaaatttta gattcaattg 1680  
aagattcaaa aaaattagga cttgacaaat ttatttttgc tttatctata aaacacatag 1740  
gacaaaaagt tgcaagtttt ataacttcta aagttcaaaa actttctgag tttctaactt 1800  
ttgattttga ttctttaatt caatataatg aaattggtcc aaaaattatt gattcagtta 1860  
aaaaatgact atcagctgaa aataataaaa aattaattaa tgactttctt aatagaggaa 1920  
tgaatttcga acatatttca aatataaaaa gcaaattatt agatggaatt aatattgtta 1980  
ttacaggaac attatctaag cctagaaatt attttgaaga attaataaaa gcaaataacg 2040  
gaaatatagt aaatagtgt tctaaaaaaa cttcttatgt tttatgcgga aaaaatcctg 2100  
gatc 2104

<210> 99  
<211> 642  
<212> PRT  
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)  
<220>  
<221> MISC\_FEATURE  
<222> (1)..(642)  
<223> Corresponds to SEQ ID NO:98, nucleotides 180..>2104  
Hypothetical DNA ligase  
Product = "7gdorfli"

<400> 99

Met Asn Ala Lys Glu Lys Asn Ile Arg Glu Glu Ile Leu Asn Leu Gln  
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Lys Lys Ile Ala Glu Trp Asp Asn Ala Tyr Tyr Asn Leu Asp Asn Pro  
20 25 30

Ile Val Thr Asp Glu Ile Tyr Asp Thr Glu Phe Ile Arg Leu Gln Lys  
35 40 45

Leu Glu Lys Gln Tyr Ser His Leu Leu Thr Tyr Glu Glu Val Lys Asn  
50 55 60

Ser Pro Thr Gln Lys Ile Asp Ala Lys Ser Leu Ser Ile Phe Asp Lys  
65 70 75 80

[illegible]

Gln Lys Phe Pro His Tyr Ala Ile Ala Phe Lys Phe Glu Pro Asn Ile  
305 310 315 320

Glu Ile Thr Thr Ile Lys Lys Ile Phe Ile Thr Ile Gly Arg Thr Gly  
325 330 335

Leu Val Thr Tyr Asn Gly Gln Val Lys Thr Val Glu Ile Ser Gly Ser  
340 345 350

Lys Ile Asn Phe Ala Thr Leu Asn Asn Phe Asn Tyr Val Lys Glu Leu  
355 360 365

Asn Leu Asn Val Gly Asp Glu Val Tyr Ile Lys Lys Ala Gly Glu Ile  
370 375 380

Ile Pro Cys Ile Ile Gly Leu Val Asn Pro Lys Gly Lys Pro Asp Tyr  
385 390 395 400

Phe Lys Arg Ile Glu Thr Cys Pro Tyr Cys Asn Ser Lys Leu Ile Glu  
405 410 415

Ser Glu Thr Phe Leu Glu Glu Tyr Cys Glu Asn Tyr Asn Cys Pro Glu  
420 425 430

Ile Ile Lys Lys Gln Leu Ile His Phe Ser Ser Lys Glu Cys Met Asn  
435 440 445

Phe Phe Ser Met Gly Glu Lys Ile Val Glu Lys Leu Tyr Glu Asn Lys  
450 455 460

Leu Ile Leu Ser Pro Leu Asp Phe Tyr Asn Leu Lys Asn Asn Lys Asn  
465 470 475 480

Glu Leu Thr Gln Leu Glu Lys Leu Gly Thr Lys Ser Ile Met Lys Ile  
485 490 495

Leu Asp Ser Ile Glu Asp Ser Lys Lys Leu Gly Leu Asp Lys Phe Ile  
500 505 510

Phe Ala Leu Ser Ile Lys His Ile Gly Gln Lys Val Ala Ser Phe Ile  
515 520 525

Thr Ser Lys Val Gln Lys Leu Ser Glu Phe Leu Thr Phe Asp Phe Asp  
530 535 540

Ser Leu Ile Gln Tyr Asn Glu Ile Gly Pro Lys Ile Ile Asp Ser Val  
545 550 555 560

Lys Lys Trp Leu Ser Ala Glu Asn Asn Lys Lys Leu Ile Asn Asp Phe  
565 570 575

Leu Asn Arg Gly Met Asn Phe Glu His Ile Ser Asn Ile Lys Ser Lys  
580 585 590

Leu Leu Asp Gly Ile Asn Ile Val Ile Thr Gly Thr Leu Ser Lys Pro  
595 600 605

Arg Asn Tyr Phe Glu Glu Leu Ile Lys Ala Asn Asn Gly Asn Ile Val  
610 615 620

Asn Ser Val Ser Lys Lys Thr Ser Tyr Val Leu Cys Gly Lys Asn Pro  
625 630 635 640

Gly Ser

<210> 100

<211> 4055

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 100

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ggacctgttc taatagctca tcttttatct ctacaacctt aataaaccat tggttactta 240

acaatatttc aataggcatt cctgatcgct cagcacattt cacattgtgt aatatttcct 300

ctttttttat cagtaaatta catttactta aggtttcaag taccagcttt cttgcttcta 360

ctattgatac tccatgtaat ttaccagata aagtatctgt ctctgcaatg ttatgtttta 420

gatcaagagt acctgattta cttattataa tctgcgtatt taaattatgt ttattccacc 480



aatatacatc taattcatca ccaaattgtac aacacattac aagaccagta cccttatcta 540  
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aggctatcgt actcataaac gatgacattt ctttttctc aacctcaact ctgctatcg 780  
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cacgtacttt ttttatcttt tcaactaaac gttctgttg caatccattg tcatcaaac 1080  
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atcaatatac aattctttta tgggtcttata taaaaactca ttataacatt cgttatatta 1680  
aataaaaaac ctataattgg gatataaaat catattacac aataacaaaa cttttataag 1740  
ttgtatcatg tacaactcat gcaaagcttg tttagtctat aatacttata ctaaataaca 1800  
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agatatatca gtaacatctt ataagaacaa aaactctaca aattacatta tttaaaatta 1920  
ataaacaat tttttagtat agtcataact caaaaatact ctagattcat aatattacac 1980  
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ttaaactatg cactgatact agatatacaa cattgtagaa ttaccttata tcttttataa	2160
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aaaccttcta agctttcatt atttttctct tagaacataa ctttacta atacgcacta	2640
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ctaccacat ataaaaaat acacacatat aaaattataa actagagaga aaaataccac	3000
aataaatcaa aagtcacaca accaattatt cactaagatt atataactct gccaaactata	3060
tcaacaaaag cctaactact gataaacact atatctatat ataaaattat aaatctagat	3120
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taactacaac taaaaactcc ctcccaccaa taaaaccata aaacctatat agacaaaata	3300
ctaataacaa accaaaagct acataactga gttattcatt aacattagct accaaagttt	3360
aatcttgatt cattataata tctgcctacc atacttataa aaactcaact acagttaaaa	3420
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tatcaataaa ttttaataat aagctactac cgatcaaaaa cttcaactgc agcagccaat	3540
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acatctacaa aatcacaacc tacagaattt aggttagaga atttatcttt aacagtatta	3660
tacctatata aataacacga aggagtatca cctatgaaat atactaatgg ttctgcagta	3720
taaccattaa acaactcttc agtcattata cttcttgta ttattacag ctcaactatt	3780

ttcctatcct taattctttt catcttattg cgattttttt tatttaactt caatatgtca 3840  
 tcaccacaat atgctacaat aattcccatt ccatatgttc cattatctgc ttttacaaac 3900  
 acatacgggt gttctgtaat actgtataat tgaaatttat tacgtatttc ttgaatcata 3960  
 acatcaactt tatcagcaat gtgttctact ccataattac ttaaaaaaca gatgttatca 4020  
 caactagaaa ataatgtaga aatcaaccaa ggatc 4055

<210> 101  
 <211> 603  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
 <221> CDS  
 <222> (1)..(603)  
 <223> Corresponds to SEQ ID NO:100, nucleotides <1..605  
 Product = "3hworf2i"

<400> 101  
 tct att ggt agt tca ttc aca tct gga ata ata atc tct tca tta tct 48  
 Ser Ile Gly Ser Ser Phe Thr Ser Gly Ile Ile Ile Ser Ser Leu Ser  
 1 5 10 15  
 ctt ttc gaa tac cat acc gga aac ggg att cca aaa tac ctt tgt cgc 96  
 Leu Phe Glu Tyr His Thr Gly Asn Gly Ile Pro Lys Tyr Leu Cys Arg  
 20 25 30  
 gat atg cac cag tcc cag ttt aac cca tct atc cac att tct att tgc 144  
 Asp Met His Gln Ser Gln Phe Asn Pro Ser Ile His Ile Ser Ile Cys  
 35 40 45  
 tta cgc ata gac tgt gga tac caa tta atc tta cgg acc tgt tct aat 192  
 Leu Arg Ile Asp Cys Gly Tyr Gln Leu Ile Leu Arg Thr Cys Ser Asn  
 50 55 60  
 agc tca tct ttt atc tct aca acc tta ata aac cat tgg tta ctt aac 240  
 Ser Ser Ser Phe Ile Ser Thr Thr Leu Ile Asn His Trp Leu Leu Asn  
 65 70 75 80  
 aat att tca ata ggc att cct gat cgc tca gca cat ttc aca ttg tgt 288  
 Asn Ile Ser Ile Gly Ile Pro Asp Arg Ser Ala His Phe Thr Leu Cys  
 85 90 95  
 aat att tcc tct ttt ttt atc agt aaa tta cat tta ctt aag gtt tca 336  
 Asn Ile Ser Ser Phe Phe Ile Ser Lys Leu His Leu Leu Lys Val Ser  
 100 105 110  
 agt acc agc ttt ctt gct tct act att gat act cca tgt aat tta cca 384  
 Ser Thr Ser Phe Leu Ala Ser Thr Ile Asp Thr Pro Cys Asn Leu Pro

115	120	125	
gat aaa gta tct gtc tct gca atg tta tgt tta aga tca aga gta cct			432
Asp Lys Val Ser Val Ser Ala Met Leu Cys Leu Arg Ser Arg Val Pro			
130	135	140	
gat tta ctt att ata atc tgc gta ttt aaa tta tgt tta ttc cac caa			480
Asp Leu Leu Ile Ile Ile Cys Val Phe Lys Leu Cys Leu Phe His Gln			
145	150	155	160
tat aca tct aat tca tca cca aat gta caa cac att aca aga cca gta			528
Tyr Thr Ser Asn Ser Ser Pro Asn Val Gln His Ile Thr Arg Pro Val			
165	170	175	
ccc tta tct att ttt act tgt tca tct gat aaa atc ggt act tta ttc			576
Pro Leu Ser Ile Phe Thr Cys Ser Ser Asp Lys Ile Gly Thr Leu Phe			
180	185	190	
cca aat ata ggt act ata gca tac tga			603
Pro Asn Ile Gly Thr Ile Ala Tyr			
195	200		

<210> 102  
 <211> 200  
 <212> PRT  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)  
 <400> 102

Ser Ile Gly Ser Ser Phe Thr Ser Gly Ile Ile Ile Ser Ser Leu Ser			
1	5	10	15
Leu Phe Glu Tyr His Thr Gly Asn Gly Ile Pro Lys Tyr Leu Cys Arg			
20	25	30	
Asp Met His Gln Ser Gln Phe Asn Pro Ser Ile His Ile Ser Ile Cys			
35	40	45	
Leu Arg Ile Asp Cys Gly Tyr Gln Leu Ile Leu Arg Thr Cys Ser Asn			
50	55	60	
Ser Ser Ser Phe Ile Ser Thr Thr Leu Ile Asn His Trp Leu Leu Asn			
65	70	75	80
Asn Ile Ser Ile Gly Ile Pro Asp Arg Ser Ala His Phe Thr Leu Cys			
85	90	95	
Asn Ile Ser Ser Phe Phe Ile Ser Lys Leu His Leu Leu Lys Val Ser			

100

105

110

Ser Thr Ser Phe Leu Ala Ser Thr Ile Asp Thr Pro Cys Asn Leu Pro  
 115 120 125

Asp Lys Val Ser Val Ser Ala Met Leu Cys Leu Arg Ser Arg Val Pro  
 130 135 140

Asp Leu Leu Ile Ile Ile Cys Val Phe Lys Leu Cys Leu Phe His Gln  
 145 150 155 160

Tyr Thr Ser Asn Ser Ser Pro Asn Val Gln His Ile Thr Arg Pro Val  
 165 170 175

Pro Leu Ser Ile Phe Thr Cys Ser Ser Asp Lys Ile Gly Thr Leu Phe  
 180 185 190

Pro Asn Ile Gly Thr Ile Ala Tyr  
 195 200

<210> 103  
 <211> 1321  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
 <221> misc\_feature  
 <222> (1)..(1321)  
 <223> n = a, c, g, or t

<220>  
 <221> misc\_feature  
 <222> (1)..(1321)  
 <223> Complement to SEQ ID NO:100, nucleotides <1..1321  
 Hypothetical valine-tRNA ligase  
 Product = "3hworfli"

<400> 103  
 ngatctattg gtagttcatt cacatctgga ataataatct cttcattatc tcttttcgaa 60  
 taccataccg gaaacgggat tccaaaatac ctttgctcgcg atatgcacca gtcccagttt 120  
 aacccatcta tccacatttc tatttgctta cgcatagact gtggatacca attaattcta 180  
 cggacctgtt ctaatagctc atctttttatc tctacaacct taataaacca ttgggttactt 240

aacaatattt caataggcat tcctgatcgc tcagcacatt tcacattgtg taatatttcc 300  
tcttttttta tcagtaaatt acatttactt aaggtttcaa gtaccagctt tottgcttct 360  
actattgata ctccatgtaa tttaccagat aaagtatctg tctctgcaat gttatgttta 420  
agatcaagag tacctgattt acttattata atctgcgtat tttaaattatg tttattccac 480  
caatatacat ctaattcatc accaaatgta caacacatta caagaccagt acccttatct 540  
atTTTTactt gttcatctga taaaatcggc actttattcc caaatatagg tactatagca 600  
tactgacctt gaagatgctg atatcttata tccaatggat taaaaataa agcaacacaa 660  
gctggcatta attctggacg cgtcgttgca atatttatta gctctccagc ctccgtagaa 720  
aaggctatcg tactcataaa cgatgacatt tccttttccct caacctcaac tctcgtatc 780  
gccgttctat cagcacaatc ccaaaatata ggctgtaact tcctatatat tttaccata 840  
ttatatagtg ctataaatga catttgagat aacttttgaa tctcttcact tatagtatga 900  
tattccagat cccaatcata actaatacca agagattgaa acaatatttt aaattccatt 960  
ctgaattttg cagatacttc attacataat gccttaaatt ctttacgac c aatatctgtc 1020  
gcacgtactt tttttatctt ttcaactaaa cgttctgttg gcaatccatt gtcacaaat 1080  
cctattggat atagtacatc ttttcctaac atacgttgat atcttgcaat aaaatccgta 1140  
tgacagtagc taaaaacatg tcctatatgt agttgtcctg atattgttgg aggaggagta 1200  
tcaataataa actggttatc ttgtaaatc ttccatttat ataattttat tttatcccaa 1260  
taggtattaa gtttttcttc tgtatctttg aacttgatt tattactaaa aagagactgc 1320  
a 1321

<210> 104  
<211> 549  
<212> DNA  
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
<221> misc\_feature  
<222> (1)..(549)  
<223> Complement to SEQ ID NO:100, nucleotides 3508..>4055  
Hypothetical glutamate-cysteine ligase  
Product = "3hworf3i"

<400> 104  
ctaccgatca aaaacttcaa ctgcagcagc caatgcagcc atcttagcaa ccatactcca 60

acagaatatt ttaccttctt gctctctaaa acttacatct acaaaatcac aacctacaga 120  
 atttaggtta gagaatttat ctttaacagt attataccta tataaataac acgaaggagt 180  
 atcacctatg aaatatacta atgggtctgc agtataacca ttaaacaact cttcagtcac 240  
 tataccttct tgtattatta cacgctcaac tattttccta tccttaattc ttttcacctt 300  
 attgcgattt tttttattta acttcaatat gtcacacca caatatgcta caataattcc 360  
 cattccatat gttccattat ctgcttttac aaacacatac ggttggtctg taatactgta 420  
 taattgaaat ttattacgta tttcttgaat cataacatca actttatcag caatgtgttc 480  
 tactccataa ttacttaaaa aacagatggt atcacaaacta gaaaataatg tagaaatcaa 540  
 ccaaggatc 549

<210> 105

<211> 4122

<212> DNA

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 105

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 agctcctacc gttttattat ggtgatactt tccttcaatt tttcctactg caccattaaa 120  
 aaatatctct ctcatgaatt aacttcctta aaaattgagt aaaccttcac ctcatcaata 180  
 atacaaaaaa gtttaactta ataaagtatt ttaacaagt gtattattaa ttacaccttc 240  
 aaaagcgcta tagttttgct ttcatttttg taaaaaaaat taaagttgca atttaaatac 300  
 atatttaaca ataaatattt ttacttatct catttaagaa aaaacctact tgacacaagg 360  
 tatattaatg atacattatc aagttgttga taatatcaaa atgatctatt caattaaaaa 420  
 tacttaaaaa ggcccataat taacgtgtgg atatttatat gttgatcaca gctaggctac 480  
 gttatgctat aatgtttatg gtaaaattgg ctcatggctt ttgcacgcaa caaaataagt 540  
 tgcaaccagt aagaatgtca tatattgcaa gtaatcaatc tttatctgaa ggatatcttg 600  
 aacaggtaat tgttcaatta aagaaaaaag ggcttattaa tgctacaaaa ggtccagggtg 660  
 gtggttattc actaagtatt gtcctcatt taattacact tagtcttata cttgaatcaa 720  
 taggcgaaaa tattaaaatt acaagatgcg aaaataacag tccaggttgt ctatcgaata 780  
 ataatagatg tgtaactcac aaattatggg atgatatagg aaattatata aaagattatt 840  
 taaataatat ttcactagag gatatagtaa ataataattt taggtcaaac atagcactac 900

ataaaaacga ggaaccctat atatatgctg attacaattc aacatctacg atactacctg 960  
 aagtaaaata tcaattgaat aatttatcct atataaaatt atataatcca tcttcaatac 1020  
 ataaactagg tcaaaaaaca aaaagtataa tagaagaaac aagaaacata gctattaagc 1080  
 aactaaatgc acaatattat gatgtagttt ttacatcctc tggtagacagaa gcaaacaatt 1140  
 tagtcatcaa tagtacatca gactataaac atttaatttc ttctacagaa catctatcta 1200  
 ttataaaatg tgctactaat gcagaattaa tacctgttga ttctaattgga ataatatgtc 1260  
 taaatgcatt gagtagtctt ttacataagt ttaaagatga caaaatacta gtatcagtaa 1320  
 tgacagcaaa caatgaaact ggtgctattc aaccaataaa aaaaatcgta gaactatcac 1380  
 ataaatttg agcattagta cacacagatg ccatacaagc gtgtggaaaa atccatatag 1440  
 atattgaaga tttaggagtt gatttggtta caatatcatc acataaactt ggcagcattg 1500  
 ctggagcagg agtggtattc tttaatagca aaaagataaa tataaaacct atgataattg 1560  
 gtggacatca agagaaagga ttaagagcag gaactgaaaa tgttttagcg atatacttat 1620  
 tatctatatc acttagtaat ttatataaat ctataacaaa gatgcttctt gttgaaaaat 1680  
 taagaaataa attggaaaat gaaatattat ctttagttcc taacgctcaa atatttagta 1740  
 gaaatgtcga gagactacca aatactagtt gtatttcaat gccaaatgta aatagtgaga 1800  
 ttcaagtaat aagctttgac ataaaaaata ttgcagtagg taacgggtca gcatgttcca 1860  
 caggagtagt agaaccctct catgtgttat ctgcaatggg ggtaaatcag gagattgcaa 1920  
 ataattcaat aaggattagc ttaagtcctg acactacaga tgagcatata agaactatag 1980  
 taaactggtg gtacgaaata tatacacata atcaagtgc taaatgaaat taggtgtaaa 2040  
 atgatgcaaa aattagaaga ttactatatc attaacgata tcaaaaatag gttataacat 2100  
 ggaaaaaata aaagatatac aacgacatat taatctacct atatttcttg attatcaatc 2160  
 cacaactaaa acggatagta gagtcttaga tgctatgatt ccatattttc aagagttttc 2220  
 taatcctcat tcacgtagtc attgttttgg atggaaagct gagtcggctg ttgaattagc 2280  
 acgagaaaga attgcatctt taataaatgc tgaaagtaaa gaagtaatat tcacttctgg 2340  
 tgctacagaa tcaataaatt tggcaattaa aggtgtagca aacttttata aaagtaaagg 2400  
 aaatcacatt attacagtac gtacagagca taaatgtggt ttagattcat gtcgccattt 2460  
 agaaacagaa ggatttgacg ttacttactt agatgtacaa aaaaatggta ttttagatct 2520  
 taatttatta aaatcagcta taactgataa gactatatgt gtatcgggta tgatggtaaa 2580



caatgaaatt ggtgtcattc aaccaataga ggaaatagga aaaatttgtc ataatcatgg 2640  
 agtattcttt catactgatg cagctcaagc atttggtaaa ataccaatag atgtaaacia 2700  
 aatgaatata gatttgctta gtatatcagg acataaaata tatgctccaa tgggaatagg 2760  
 ggcattatat gtacgtaaac gtcaaccaag aatacgactt actcctataa taaatgggtgg 2820  
 tggacaagaa cgtgggtatga gatctggaac catacctact ccattagcag taggtttagg 2880  
 ggaagcagca tatatagctc aggaagtaat ggaagatgaa gccattagga taaaagaatt 2940  
 gcgtgatatt ttatatagtg aaataaaaaa acattttacc tatgtaatac tgaatgggtga 3000  
 ttatgaacia cgtatagcag gaaatttaaa ttttaagtttt ccatatgtag aaggagaatc 3060  
 tattattatg gcgattaaca acttagcagt aagttcagga tctgcttgta catctgcttc 3120  
 actagaacca tcttatgttt tacgtgcgtt aaatatagat aaggatttag aacactcatc 3180  
 tattagattt ggaataggta ggtttactac aaaagcagaa attttatatg cagcggatct 3240  
 tattgtaaat agcataaaga ggttgcgtga gatgagtcct ttatgggaaa tgggtacaaga 3300  
 aggtataaat cttaatgaaa ttaagtggga tgtgcattaa tttttattgt atttgataat 3360  
 tatgaggtat ttatatgagt tacagtgagt ctcttctaga acattataag aatcctaaaa 3420  
 atgttggtac ttacctaata gaggattaca atgtaggtac tggcttagtg ggagctccta 3480  
 gctgtgggtga tgtaatgaag ttacagatta aagtagatga taatggaaaa attatagatg 3540  
 caaaatttaa aacttttggg tgtgggtgctg caattgcagc tagttcacta gctactgagt 3600  
 taattaaagg taaaacagta gatgaggcac atgagttgaa aaatacagta ttggcaaaag 3660  
 aattaagttt acctccagtg aaaatacatt gttcattact tgcagaagat gctgtaaaag 3720  
 cagctataaa tgactatcat atgaaacaag caaacaaaaa aaatgctact aaagatccta 3780  
 atgaataata cagcaataat atgcaatcag gtttatctat ggataaagaa gtgttgatac 3840  
 cacataataa tcaagagaat acatgtgatt cacagataaa gtattttata aacagtagtt 3900  
 tcacagataa gtctcctatt atcataacgg aaaatgctat taaaaaaatt aaggaactca 3960  
 ttgataagaa aaaagattct gtcattggga ttagaataat ggtagcgcaa aaaggatggt 4020  
 ttggttttta gtataatata gaatatgcat atgatatcaa aatgttagat gtacaaattc 4080  
 aagtaaaata tcaaaatcaa aattttataa ttttgattga tc 4122

<210> 106

<211> 1569  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<220>  
 <221> CDS  
 <222> (1)..(1569)  
 <223> Corresponds to SEQ ID NO:105, nucleotides 459..2027  
 Hypothetical iron-sulfur co-factor synthesis  
 Product = "11hworf1"

<400> 106  
 atg ttg atc aca gct agg cta cgt tat gct ata atg ttt atg gta aaa 48  
 Met Leu Ile Thr Ala Arg Leu Arg Tyr Ala Ile Met Phe Met Val Lys  
 1 5 10 15

ttg gct cat ggt ctt tgc acg caa caa aat aag ttg caa cca gta aga 96  
 Leu Ala His Gly Leu Cys Thr Gln Gln Asn Lys Leu Gln Pro Val Arg  
 20 25 30

atg tca tat att gca agt aat caa tct tta tct gaa gga tat ctt gaa 144  
 Met Ser Tyr Ile Ala Ser Asn Gln Ser Leu Ser Glu Gly Tyr Leu Glu  
 35 40 45

cag gta att gtt caa tta aag aaa aaa ggg ctt att aat gct aca aaa 192  
 Gln Val Ile Val Gln Leu Lys Lys Lys Gly Leu Ile Asn Ala Thr Lys  
 50 55 60

ggc cca ggt ggt ggt tat tca cta agt att gct cct cat tta att aca 240  
 Gly Pro Gly Gly Gly Tyr Ser Leu Ser Ile Ala Pro His Leu Ile Thr  
 65 70 75 80

ctt agt ctt ata ctt gaa tca ata ggc gaa aat att aaa att aca aga 288  
 Leu Ser Leu Ile Leu Glu Ser Ile Gly Glu Asn Ile Lys Ile Thr Arg  
 85 90 95

tgc gaa aat aac agt cca ggt tgt cta tcg aat aat aat aga tgt gta 336  
 Cys Glu Asn Asn Ser Pro Gly Cys Leu Ser Asn Asn Asn Arg Cys Val  
 100 105 110

act cac aaa tta tgg gat gat ata gga aat tat ata aaa gat tat tta 384  
 Thr His Lys Leu Trp Asp Asp Ile Gly Asn Tyr Ile Lys Asp Tyr Leu  
 115 120 125

aat aat att tca cta gag gat ata gta aat aat aat ttt agg tca aac 432  
 Asn Asn Ile Ser Leu Glu Asp Ile Val Asn Asn Asn Phe Arg Ser Asn  
 130 135 140

ata gca cta cat aaa aac gag gaa ccc tat ata tat gct gat tac aat 480  
 Ile Ala Leu His Lys Asn Glu Glu Pro Tyr Ile Tyr Ala Asp Tyr Asn  
 145 150 155 160

tca aca tct acg ata cta cct gaa gta aaa tat caa ttg aat aat tta 528  
 Ser Thr Ser Thr Ile Leu Pro Glu Val Lys Tyr Gln Leu Asn Asn Leu

	165	170	175	
tcc tat ata aaa tta tat aat cca tct tca ata cat aaa cta ggt caa				576
Ser Tyr Ile Lys Leu Tyr Asn Pro Ser Ser Ile His Lys Leu Gly Gln				
	180	185	190	
aaa aca aaa agt ata ata gaa gaa aca aga aac ata gct att aag caa				624
Lys Thr Lys Ser Ile Ile Glu Glu Thr Arg Asn Ile Ala Ile Lys Gln				
	195	200	205	
cta aat gca caa tat tat gat gta gtt ttt aca tcc tct ggt aca gaa				672
Leu Asn Ala Gln Tyr Tyr Asp Val Val Phe Thr Ser Ser Gly Thr Glu				
	210	215	220	
gca aac aat tta gtc atc aat agt aca tca gac tat aaa cat tta att				720
Ala Asn Asn Leu Val Ile Asn Ser Thr Ser Asp Tyr Lys His Leu Ile				
	225	230	235	240
tct tct aca gaa cat cta tct att ata aaa tgt gct act aat gca gaa				768
Ser Ser Thr Glu His Leu Ser Ile Ile Lys Cys Ala Thr Asn Ala Glu				
	245	250	255	
tta ata cct gtt gat tct aat gga ata ata tgt cta aat gca ttg agt				816
Leu Ile Pro Val Asp Ser Asn Gly Ile Ile Cys Leu Asn Ala Leu Ser				
	260	265	270	
agt ctt tta cat aag ttt aaa gat gac aaa ata cta gta tca gta atg				864
Ser Leu Leu His Lys Phe Lys Asp Asp Lys Ile Leu Val Ser Val Met				
	275	280	285	
aca gca aac aat gaa act ggt gct att caa cca ata aaa aaa atc gta				912
Thr Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Ile Lys Lys Ile Val				
	290	295	300	
gaa cta tca cat aaa ttt gga gca tta gta cac aca gat gcc ata caa				960
Glu Leu Ser His Lys Phe Gly Ala Leu Val His Thr Asp Ala Ile Gln				
	305	310	315	320
gcg tgt gga aaa atc cat ata gat att gaa gat tta gga gtt gat ttg				1008
Ala Cys Gly Lys Ile His Ile Asp Ile Glu Asp Leu Gly Val Asp Leu				
	325	330	335	
tta aca ata tca tca cat aaa ctt ggc agc att gct gga gca gga gtg				1056
Leu Thr Ile Ser Ser His Lys Leu Gly Ser Ile Ala Gly Ala Gly Val				
	340	345	350	
tta ttc ttt aat agc aaa aag ata aat ata aaa cct atg ata att ggt				1104
Leu Phe Phe Asn Ser Lys Lys Ile Asn Ile Lys Pro Met Ile Ile Gly				
	355	360	365	
gga cat caa gag aaa gga tta aga gca gga act gaa aat gtt tta gcg				1152
Gly His Gln Glu Lys Gly Leu Arg Ala Gly Thr Glu Asn Val Leu Ala				
	370	375	380	
ata tac tta tta tct ata tca ctt agt aat tta tat aaa tct ata aca				1200

Ile Tyr Leu Leu Ser Ile Ser Leu Ser Asn Leu Tyr Lys Ser Ile Thr  
 385 390 395 400  
 aag atg ctt ctt gtt gaa aaa tta aga aat aaa ttg gaa aat gaa ata 1248  
 Lys Met Leu Leu Val Glu Lys Leu Arg Asn Lys Leu Glu Asn Glu Ile  
 405 410 415  
 tta tct tta gtt cct aac gct caa ata ttt agt aga aat gtc gag aga 1296  
 Leu Ser Leu Val Pro Asn Ala Gln Ile Phe Ser Arg Asn Val Glu Arg  
 420 425 430  
 cta cca aat act agt tgt att tca atg cca aat gta aat agt gag att 1344  
 Leu Pro Asn Thr Ser Cys Ile Ser Met Pro Asn Val Asn Ser Glu Ile  
 435 440 445  
 caa gta ata agc ttt gac ata aaa aat att gca gta ggt aac ggg tca 1392  
 Gln Val Ile Ser Phe Asp Ile Lys Asn Ile Ala Val Gly Asn Gly Ser  
 450 455 460  
 gca tgt tcc aca gga gta gta gaa ccc tct cat gtg tta tct gca atg 1440  
 Ala Cys Ser Thr Gly Val Val Glu Pro Ser His Val Leu Ser Ala Met  
 465 470 475 480  
 ggg gta aat cag gag att gca aat aat tca ata agg att agc tta agt 1488  
 Gly Val Asn Gln Glu Ile Ala Asn Asn Ser Ile Arg Ile Ser Leu Ser  
 485 490 495  
 cct gac act aca gat gag cat ata aga act ata gta aac tgt tgg tac 1536  
 Pro Asp Thr Thr Asp Glu His Ile Arg Thr Ile Val Asn Cys Trp Tyr  
 500 505 510  
 gaa ata tat aca cat aat caa gtg cat aaa tga 1569  
 Glu Ile Tyr Thr His Asn Gln Val His Lys  
 515 520

<210> 107  
 <211> 522  
 <212> PRT  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 107

Met Leu Ile Thr Ala Arg Leu Arg Tyr Ala Ile Met Phe Met Val Lys  
 1 5 10 15

Leu Ala His Gly Leu Cys Thr Gln Gln Asn Lys Leu Gln Pro Val Arg  
 20 25 30

Met Ser Tyr Ile Ala Ser Asn Gln Ser Leu Ser Glu Gly Tyr Leu Glu  
 35 40 45

Gln Val Ile Val Gln Leu Lys Lys Lys Gly Leu Ile Asn Ala Thr Lys  
50 55 60

Gly Pro Gly Gly Gly Tyr Ser Leu Ser Ile Ala Pro His Leu Ile Thr  
65 70 75 80

Leu Ser Leu Ile Leu Glu Ser Ile Gly Glu Asn Ile Lys Ile Thr Arg  
85 90 95

Cys Glu Asn Asn Ser Pro Gly Cys Leu Ser Asn Asn Asn Arg Cys Val  
100 105 110

Thr His Lys Leu Trp Asp Asp Ile Gly Asn Tyr Ile Lys Asp Tyr Leu  
115 120 125

Asn Asn Ile Ser Leu Glu Asp Ile Val Asn Asn Asn Phe Arg Ser Asn  
130 135 140

Ile Ala Leu His Lys Asn Glu Glu Pro Tyr Ile Tyr Ala Asp Tyr Asn  
145 150 155 160

Ser Thr Ser Thr Ile Leu Pro Glu Val Lys Tyr Gln Leu Asn Asn Leu  
165 170 175

Ser Tyr Ile Lys Leu Tyr Asn Pro Ser Ser Ile His Lys Leu Gly Gln  
180 185 190

Lys Thr Lys Ser Ile Ile Glu Glu Thr Arg Asn Ile Ala Ile Lys Gln  
195 200 205

Leu Asn Ala Gln Tyr Tyr Asp Val Val Phe Thr Ser Ser Gly Thr Glu  
210 215 220

Ala Asn Asn Leu Val Ile Asn Ser Thr Ser Asp Tyr Lys His Leu Ile  
225 230 235 240

Ser Ser Thr Glu His Leu Ser Ile Ile Lys Cys Ala Thr Asn Ala Glu  
245 250 255

Leu Ile Pro Val Asp Ser Asn Gly Ile Ile Cys Leu Asn Ala Leu Ser  
260 265 270

Ser Leu Leu His Lys Phe Lys Asp Asp Lys Ile Leu Val Ser Val Met  
275 280 285

Thr Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Ile Lys Lys Ile Val  
290 295 300

Glu Leu Ser His Lys Phe Gly Ala Leu Val His Thr Asp Ala Ile Gln  
305 310 315 320

Ala Cys Gly Lys Ile His Ile Asp Ile Glu Asp Leu Gly Val Asp Leu  
325 330 335

Leu Thr Ile Ser Ser His Lys Leu Gly Ser Ile Ala Gly Ala Gly Val  
340 345 350

Leu Phe Phe Asn Ser Lys Lys Ile Asn Ile Lys Pro Met Ile Ile Gly  
355 360 365

Gly His Gln Glu Lys Gly Leu Arg Ala Gly Thr Glu Asn Val Leu Ala  
370 375 380

Ile Tyr Leu Leu Ser Ile Ser Leu Ser Asn Leu Tyr Lys Ser Ile Thr  
385 390 395 400

Lys Met Leu Leu Val Glu Lys Leu Arg Asn Lys Leu Glu Asn Glu Ile  
405 410 415

Leu Ser Leu Val Pro Asn Ala Gln Ile Phe Ser Arg Asn Val Glu Arg  
420 425 430

Leu Pro Asn Thr Ser Cys Ile Ser Met Pro Asn Val Asn Ser Glu Ile  
435 440 445

Gln Val Ile Ser Phe Asp Ile Lys Asn Ile Ala Val Gly Asn Gly Ser  
450 455 460

Ala Cys Ser Thr Gly Val Val Glu Pro Ser His Val Leu Ser Ala Met  
465 470 475 480

Gly Val Asn Gln Glu Ile Ala Asn Asn Ser Ile Arg Ile Ser Leu Ser  
485 490 495

Pro Asp Thr Thr Asp Glu His Ile Arg Thr Ile Val Asn Cys Trp Tyr  
 500 505 510

Glu Ile Tyr Thr His Asn Gln Val His Lys  
 515 520

<210> 108  
 <211> 1242  
 <212> DNA  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)  
 <220>  
 <221> CDS  
 <222> (1)..(1242)  
 <223> Corresponds to SEQ ID NO:105, nucleotides 2099..3340  
 Hypothetical iron-sulfur co-factor synthesis  
 Product = "11hworf2"

<400> 108  
 atg gaa aaa ata aaa gat ata caa cga cat att aat cta cct ata ttt 48  
 Met Glu Lys Ile Lys Asp Ile Gln Arg His Ile Asn Leu Pro Ile Phe  
 1 5 10 15  
 ctt gat tat caa tcc aca act aaa acg gat agt aga gtc tta gat gct 96  
 Leu Asp Tyr Gln Ser Thr Thr Lys Thr Asp Ser Arg Val Leu Asp Ala  
 20 25 30  
 atg att cca tat ttt caa gag ttt tct aat cct cat tca cgt agt cat 144  
 Met Ile Pro Tyr Phe Gln Glu Phe Ser Asn Pro His Ser Arg Ser His  
 35 40 45  
 tgt ttt gga tgg aaa gct gag tcg gct gtt gaa tta gca cga gaa aga 192  
 Cys Phe Gly Trp Lys Ala Glu Ser Ala Val Glu Leu Ala Arg Glu Arg  
 50 55 60  
 att gca tct tta ata aat gct gaa agt aaa gaa gta ata ttc act tct 240  
 Ile Ala Ser Leu Ile Asn Ala Glu Ser Lys Glu Val Ile Phe Thr Ser  
 65 70 75 80  
 ggt gct aca gaa tca aat aat ttg gca att aaa ggt gta gca aac ttt 288  
 Gly Ala Thr Glu Ser Asn Asn Leu Ala Ile Lys Gly Val Ala Asn Phe  
 85 90 95  
 tat aaa agt aaa gga aat cac att att aca gta cgt aca gag cat aaa 336  
 Tyr Lys Ser Lys Gly Asn His Ile Ile Thr Val Arg Thr Glu His Lys  
 100 105 110  
 tgt gtt tta gat tca tgt cgc cat tta gaa aca gaa gga ttt gac gtt 384  
 Cys Val Leu Asp Ser Cys Arg His Leu Glu Thr Glu Gly Phe Asp Val  
 115 120 125

act tac tta gat gta caa aaa aat ggt att tta gat ctt aat tta tta 432  
 Thr Tyr Leu Asp Val Gln Lys Asn Gly Ile Leu Asp Leu Asn Leu Leu  
 130 135 140

aaa tca gct ata act gat aag act ata ttg gta tcg gtt atg atg gta 480  
 Lys Ser Ala Ile Thr Asp Lys Thr Ile Leu Val Ser Val Met Met Val  
 145 150 155 160

aac aat gaa att ggt gtc att caa cca ata gag gaa ata gga aaa att 528  
 Asn Asn Glu Ile Gly Val Ile Gln Pro Ile Glu Glu Ile Gly Lys Ile  
 165 170 175

tgt cat aat cat gga gta ttc ttt cat act gat gca gct caa gca ttt 576  
 Cys His Asn His Gly Val Phe Phe His Thr Asp Ala Ala Gln Ala Phe  
 180 185 190

ggt aaa ata cca ata gat gta aac aaa atg aat ata gat ttg ctt agt 624  
 Gly Lys Ile Pro Ile Asp Val Asn Lys Met Asn Ile Asp Leu Leu Ser  
 195 200 205

ata tca gga cat aaa ata tat gct cca atg gga ata ggg gca tta tat 672  
 Ile Ser Gly His Lys Ile Tyr Ala Pro Met Gly Ile Gly Ala Leu Tyr  
 210 215 220

gta cgt aaa cgt caa cca aga ata cga ctt act cct ata ata aat ggt 720  
 Val Arg Lys Arg Gln Pro Arg Ile Arg Leu Thr Pro Ile Ile Asn Gly  
 225 230 235 240

ggt gga caa gaa cgt ggt atg aga tct gga acc ata cct act cca tta 768  
 Gly Gly Gln Glu Arg Gly Met Arg Ser Gly Thr Ile Pro Thr Pro Leu  
 245 250 255

gca gta ggt tta ggg gaa gca gca tat ata gct cag gaa gta atg gaa 816  
 Ala Val Gly Leu Gly Glu Ala Ala Tyr Ile Ala Gln Glu Val Met Glu  
 260 265 270

gat gaa gcc att agg ata aaa gaa ttg cgt gat att tta tat agt gaa 864  
 Asp Glu Ala Ile Arg Ile Lys Glu Leu Arg Asp Ile Leu Tyr Ser Glu  
 275 280 285

ata aaa aaa cat tta ccc tat gta ata ctg aat ggt gat tat gaa caa 912  
 Ile Lys Lys His Leu Pro Tyr Val Ile Leu Asn Gly Asp Tyr Glu Gln  
 290 295 300

cgt ata gca gga aat tta aat tta agt ttt cca tat gta gaa gga gaa 960  
 Arg Ile Ala Gly Asn Leu Asn Leu Ser Phe Pro Tyr Val Glu Gly Glu  
 305 310 315 320

tct att att atg gcg att aac aac tta gca gta agt tca gga tct gct 1008  
 Ser Ile Ile Met Ala Ile Asn Asn Leu Ala Val Ser Ser Gly Ser Ala  
 325 330 335

tgt aca tct gct tca cta gaa cca tct tat gtt tta cgt gcg tta aat 1056  
 Cys Thr Ser Ala Ser Leu Glu Pro Ser Tyr Val Leu Arg Ala Leu Asn



340	345	350	
ata gat aag gat tta gaa cac tca tct att aga ttt gga ata ggt agg			1104
Ile Asp Lys Asp Leu Glu His Ser Ser Ile Arg Phe Gly Ile Gly Arg			
355	360	365	
ttt act aca aaa gca gaa att tta tat gca gcg gat ctt att gta aat			1152
Phe Thr Thr Lys Ala Glu Ile Leu Tyr Ala Ala Asp Leu Ile Val Asn			
370	375	380	
agc ata aag agg ttg cgt gag atg agt cct tta tgg gaa atg gta caa			1200
Ser Ile Lys Arg Leu Arg Glu Met Ser Pro Leu Trp Glu Met Val Gln			
385	390	395	400
gaa ggt ata aat ctt aat gaa att aag tgg gat gtg cat taa			1242
Glu Gly Ile Asn Leu Asn Glu Ile Lys Trp Asp Val His			
405	410		

<210> 109  
 <211> 413  
 <212> PRT  
 <213> Ehrlichia ruminantium (formerly Cowdria ruminantium)  
 <400> 109

Met Glu Lys Ile Lys Asp Ile Gln Arg His Ile Asn Leu Pro Ile Phe  
1 5 10 15

Leu Asp Tyr Gln Ser Thr Thr Lys Thr Asp Ser Arg Val Leu Asp Ala  
20 25 30

Met Ile Pro Tyr Phe Gln Glu Phe Ser Asn Pro His Ser Arg Ser His  
35 40 45

Cys Phe Gly Trp Lys Ala Glu Ser Ala Val Glu Leu Ala Arg Glu Arg  
50 55 60

Ile Ala Ser Leu Ile Asn Ala Glu Ser Lys Glu Val Ile Phe Thr Ser  
65 70 75 80

Gly Ala Thr Glu Ser Asn Asn Leu Ala Ile Lys Gly Val Ala Asn Phe  
85 90 95

Tyr Lys Ser Lys Gly Asn His Ile Ile Thr Val Arg Thr Glu His Lys  
100 105 110

Cys Val Leu Asp Ser Cys Arg His Leu Glu Thr Glu Gly Phe Asp Val

115

120

125

Thr Tyr Leu Asp Val Gln Lys Asn Gly Ile Leu Asp Leu Asn Leu Leu  
 130 135 140

Lys Ser Ala Ile Thr Asp Lys Thr Ile Leu Val Ser Val Met Met Val  
 145 150 155 160

Asn Asn Glu Ile Gly Val Ile Gln Pro Ile Glu Glu Ile Gly Lys Ile  
 165 170 175

Cys His Asn His Gly Val Phe Phe His Thr Asp Ala Ala Gln Ala Phe  
 180 185 190

Gly Lys Ile Pro Ile Asp Val Asn Lys Met Asn Ile Asp Leu Leu Ser  
 195 200 205

Ile Ser Gly His Lys Ile Tyr Ala Pro Met Gly Ile Gly Ala Leu Tyr  
 210 215 220

Val Arg Lys Arg Gln Pro Arg Ile Arg Leu Thr Pro Ile Ile Asn Gly  
 225 230 235 240

Gly Gly Gln Glu Arg Gly Met Arg Ser Gly Thr Ile Pro Thr Pro Leu  
 245 250 255

Ala Val Gly Leu Gly Glu Ala Ala Tyr Ile Ala Gln Glu Val Met Glu  
 260 265 270

Asp Glu Ala Ile Arg Ile Lys Glu Leu Arg Asp Ile Leu Tyr Ser Glu  
 275 280 285

Ile Lys Lys His Leu Pro Tyr Val Ile Leu Asn Gly Asp Tyr Glu Gln  
 290 295 300

Arg Ile Ala Gly Asn Leu Asn Leu Ser Phe Pro Tyr Val Glu Gly Glu  
 305 310 315 320

Ser Ile Ile Met Ala Ile Asn Asn Leu Ala Val Ser Ser Gly Ser Ala  
 325 330 335

200220 150300

Cys Thr Ser Ala Ser Leu Glu Pro Ser Tyr Val Leu Arg Ala Leu Asn  
340 345 350

Ile Asp Lys Asp Leu Glu His Ser Ser Ile Arg Phe Gly Ile Gly Arg  
355 360 365

Phe Thr Thr Lys Ala Glu Ile Leu Tyr Ala Ala Asp Leu Ile Val Asn  
370 375 380

Ser Ile Lys Arg Leu Arg Glu Met Ser Pro Leu Trp Glu Met Val Gln  
385 390 395 400

Glu Gly Ile Asn Leu Asn Glu Ile Lys Trp Asp Val His  
405 410

<210> 110  
<211> 414  
<212> DNA  
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)  
  
<220>  
<221> CDS  
<222> (1)..(414)  
<223> Corresponds to SEQ ID NO:105, nucleotides 3375-3788  
NIFU-like protein  
Product = "11hworf3"

<400> 110  
atg agt tac agt gag tct ctt cta gaa cat tat aag aat cct aaa aat 48  
Met Ser Tyr Ser Glu Ser Leu Leu Glu His Tyr Lys Asn Pro Lys Asn  
1 5 10 15  
  
gtt ggt act tta cct aaa gag gat tac aat gta ggt act ggc tta gtg 96  
Val Gly Thr Leu Pro Lys Glu Asp Tyr Asn Val Gly Thr Gly Leu Val  
20 25 30  
  
gga gct cct agc tgt ggt gat gta atg aag tta cag att aaa gta gat 144  
Gly Ala Pro Ser Cys Gly Asp Val Met Lys Leu Gln Ile Lys Val Asp  
35 40 45  
  
gat aat gga aaa att ata gat gca aaa ttt aaa act ttt gga tgt ggt 192  
Asp Asn Gly Lys Ile Ile Asp Ala Lys Phe Lys Thr Phe Gly Cys Gly  
50 55 60  
  
gct gca att gca gct agt tca cta gct act gag tta att aaa ggt aaa 240  
Ala Ala Ile Ala Ala Ser Ser Leu Ala Thr Glu Leu Ile Lys Gly Lys  
65 70 75 80  
  
aca gta gat gag gca cat gag ttg aaa aat aca gta ttg gca aaa gaa 288

Thr Val Asp Glu Ala His Glu Leu Lys Asn Thr Val Leu Ala Lys Glu  
85 90 95

tta agt tta cct cca gtg aaa ata cat tgt tca tta ctt gca gaa gat 336  
Leu Ser Leu Pro Pro Val Lys Ile His Cys Ser Leu Leu Ala Glu Asp  
100 105 110

gct gta aaa gca gct ata aat gac tat cat atg aaa caa gca aac aaa 384  
Ala Val Lys Ala Ala Ile Asn Asp Tyr His Met Lys Gln Ala Asn Lys  
115 120 125

aaa aat gct act aaa gat cct aat gaa taa 414  
Lys Asn Ala Thr Lys Asp Pro Asn Glu  
130 135

<210> 111

<211> 137

<212> PRT

<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 111

Met Ser Tyr Ser Glu Ser Leu Leu Glu His Tyr Lys Asn Pro Lys Asn  
1 5 10 15

Val Gly Thr Leu Pro Lys Glu Asp Tyr Asn Val Gly Thr Gly Leu Val  
20 25 30

Gly Ala Pro Ser Cys Gly Asp Val Met Lys Leu Gln Ile Lys Val Asp  
35 40 45

Asp Asn Gly Lys Ile Ile Asp Ala Lys Phe Lys Thr Phe Gly Cys Gly  
50 55 60

Ala Ala Ile Ala Ala Ser Ser Leu Ala Thr Glu Leu Ile Lys Gly Lys  
65 70 75 80

Thr Val Asp Glu Ala His Glu Leu Lys Asn Thr Val Leu Ala Lys Glu  
85 90 95

Leu Ser Leu Pro Pro Val Lys Ile His Cys Ser Leu Leu Ala Glu Asp  
100 105 110

Ala Val Lys Ala Ala Ile Asn Asp Tyr His Met Lys Gln Ala Asn Lys  
115 120 125

Lys Asn Ala Thr Lys Asp Pro Asn Glu  
130 135

<210> 112  
<211> 15  
<212> PRT  
<213> Unknown

<220>  
<223> Hypothetical sequence

<400> 112

Pro Thr Leu Val Thr Leu Ser Val Cys His Phe Gly Ile Glu Leu  
1 5 10 15

<210> 113  
<211> 13  
<212> PRT  
<213> Unknown

<220>  
<223> Hypothetical sequence

<400> 113

Leu Val Thr Leu Ser Val Cys His Phe Gly Ile Glu Leu  
1 5 10

<210> 114  
<211> 18  
<212> DNA  
<213> Unknown

<220>  
<223> Primer

<400> 114  
cggggtaccg aattcctc

18

<210> 115  
<211> 18  
<212> DNA  
<213> Unknown

<220>  
<223> Primer

<400> 115  
gcatgctcct ctagactc

18

<210> 116  
<211> 9  
<212> PRT  
<213> Ehrlichia ruminantium (formerly Cowdria ruminantium)

<400> 116

Val Thr Ser Ser Pro Glu Gly Ser Val  
1 5

<210> 117  
<211> 9  
<212> PRT  
<213> Unknown

<220>  
<223> Synthetic peptide

<400> 117

Val Thr Ser Ser Pro Glu Gly Ser Val  
1 5

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